



Fig. 1

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drIndyl sequence (total 2602)

(ORF: 258 - 1976)

SEQ ID NO: 1

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Peptide seq (total 572)

SEQ ID NO: 2

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Fig. 2A

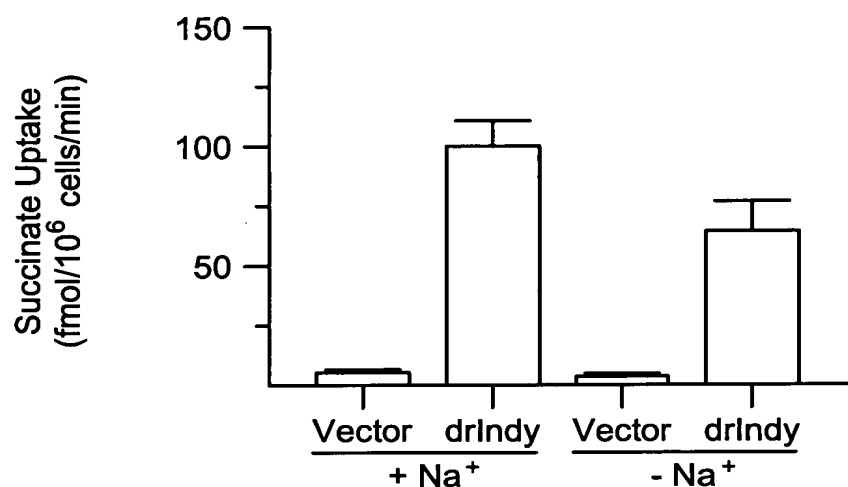
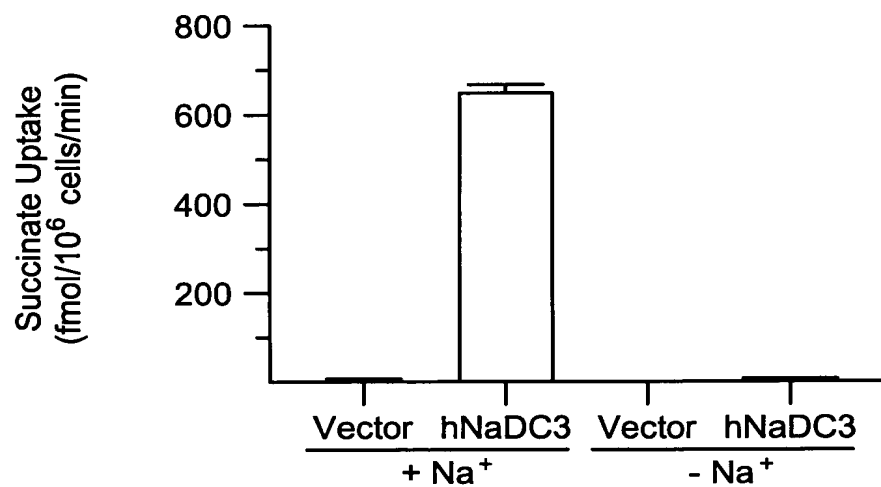
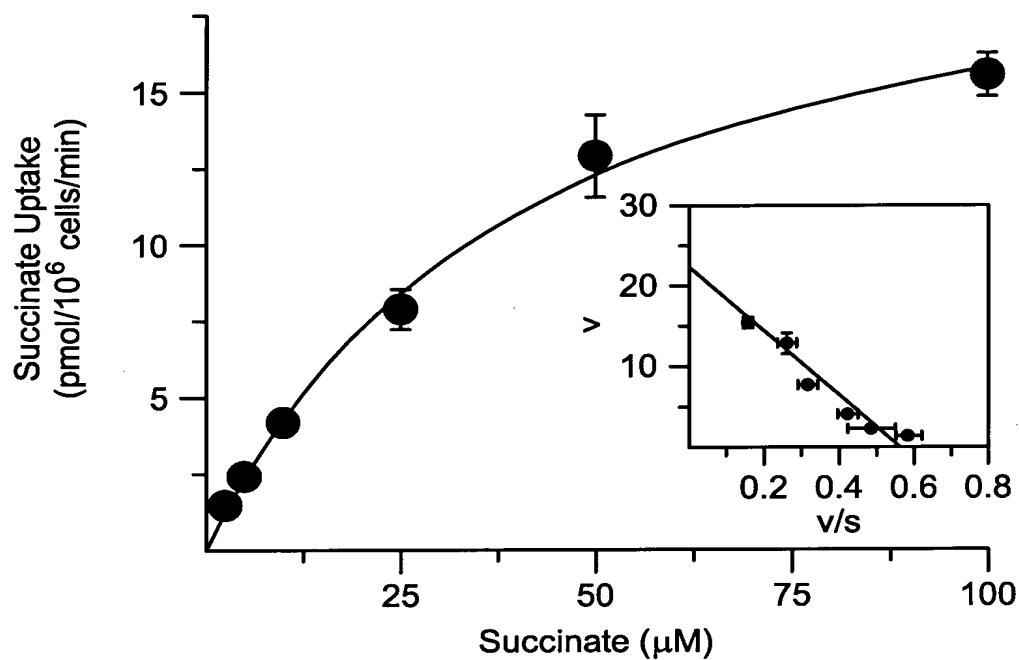


Fig. 2B



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Fig. 3



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Fig. 4A

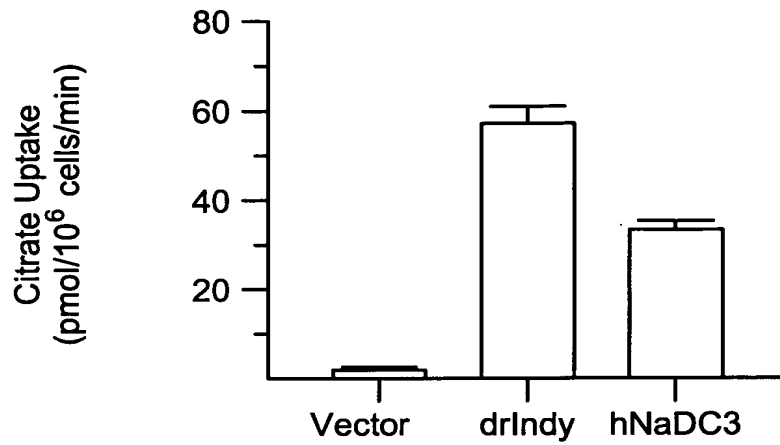
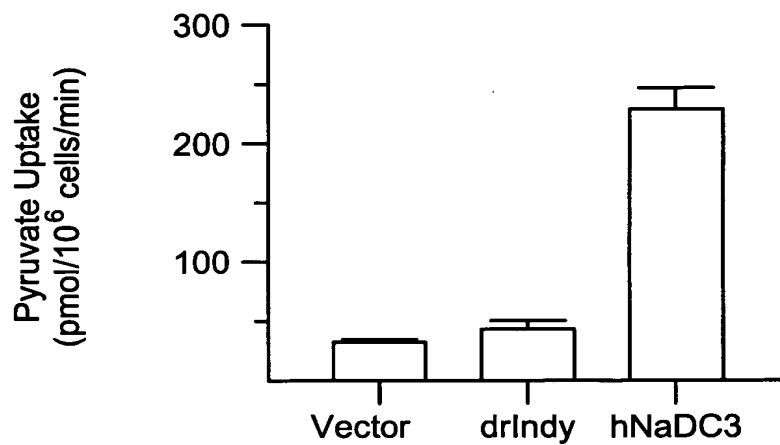
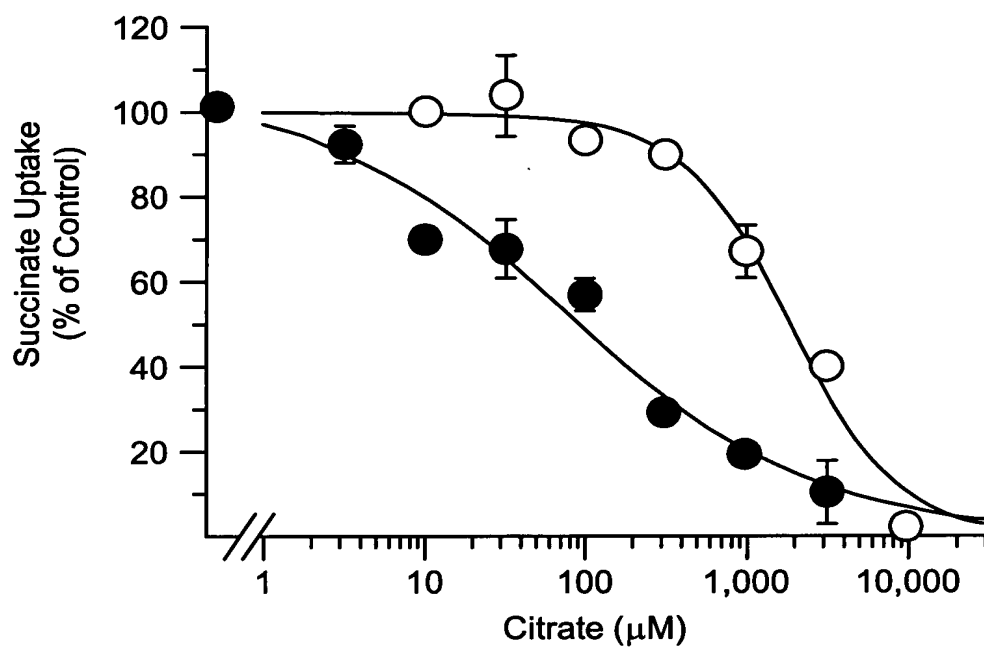


Fig. 4B



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Fig. 5



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Fig. 6A

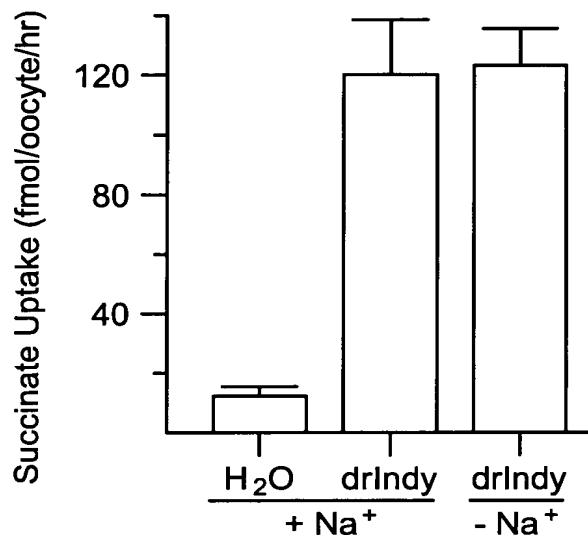


Fig. 6B

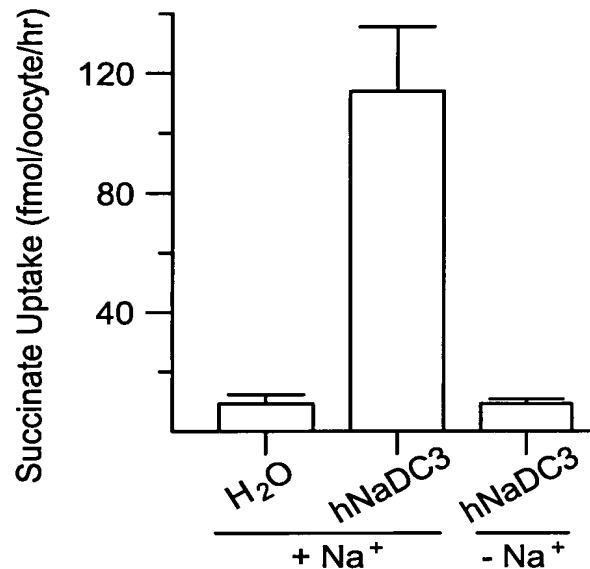
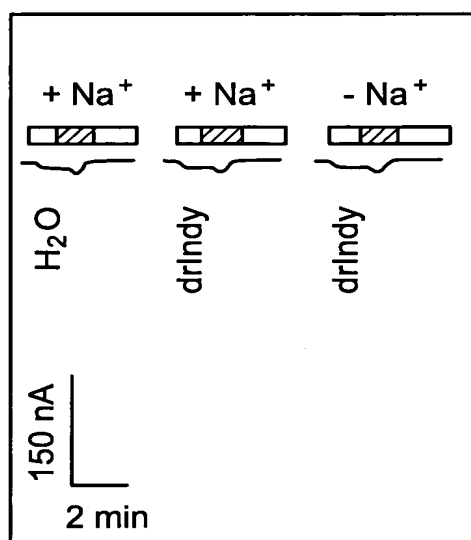
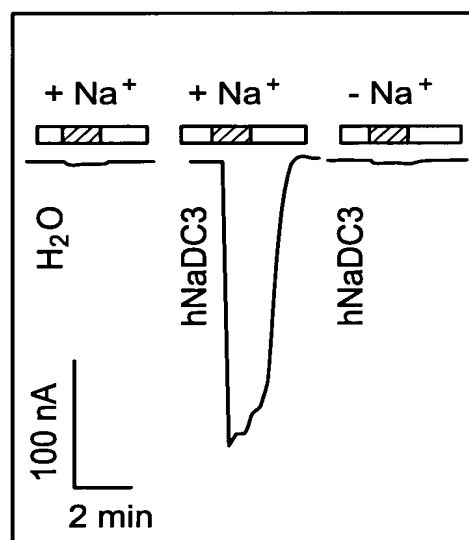


Fig. 6C



Perifusion Buffer
 2 mM Succinate

Fig. 6D



Perifusion Buffer
 2 mM Succinate

Fig. 7

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Rat INDY seq.
(3191 nt + 63 nt polyA)
SEQ ID NO: 3

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(572 aa)
SEQ ID NO: 4

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FPDWANLTHINT

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Fig. 8

rNaCT 1 ---MASAKTYVTKPKSFVILFFAPILLLPLIILVDPKFAFCAYVIILMAFYWCTDVLPVA
rNaDC1 1 ---MATCWPALWAYRFYLIIVLCPIFLLPLPLIVOTKEAYCAYSIILMALLWCTEALPLA
rNaDC3 1 MAALAALAKKVWSARRLLVLLLVPLALLPILFAUPPKEGRCYVILLMAVYWCTEALPLS

rNaCT 58 ITSLIPVILFPLKVLDSKQVCVQYMTDTNMLFLGSLIVATAVERWELHKRIALRMLLFV
rNaDC1 58 VTALFPIVLFPLMGIMDASEVCIIEYFKDTNILFVGGLMVAIAVEHWNLHKRIALQVLLII
rNaDC3 61 VTALLPIILFFPMGILPSSKVCPOYFLDTNLFSLGLIMASATEERNLHRRIALKVLMLV

rNaCT 118 GIKPSRLMLGFMFVTAFLSMWISNTATTAMMIPIVEAMLEQMVAAA---TNVAVDASQR---T
rNaDC1 118 GVRPALLLLGFMFVTAFLSMWISNTATTAMMVPIGHAVLEQLOG---SKKDVEGGNNNPT
rNaDC3 121 GVOPARLLLGMMVTTSFSLMWISNTASTAMMLPIASATLKSIFGORDTRKDLPREGEDST

rNaCT 173 MELLDKN-----KASELPGSOVVFEDPS-VKOEDEETKN-MYKAMNLCV CYAA
rNaDC1 175 FELOEECPQ-----KEVIKLDNGOPVSAPSE-PRTOKTQEHHR-FSQGLSLCICYSYA
rNaDC3 181 AAVRGNGLRTPTEMQFLASSEGGHAEDEVAPLELPDDSKEEHRRNIWKGFLLSIPYSA

rNaCT 220 SIGGTATLTGTGPNVLLGQMQLFPDSDKDVNFASFAPALPNMLLMLVMAWLWLLCFY
rNaDC1 225 SIGGIATLTGTTPNLVLOGQVNSLFPONGNVNFASFWGFAPPTMTIILLLLAWLWLVLF
rNaDC3 241 SIGGTATLTGTAPNLILLGOLKSFFPQC-DVNVFGSWTFAPPLMLLELLVGWLWISFLY

rNaCT 280 MRPNLKKTCICCGRKKKDTEKIASKVLVEEYRKLGPLSYAECNVLFCEGLLILWFSRDP
rNaDC1 285 LGVNFRKN-FGFGEGERKQAAFOVIKTQYRLLGPMSFAEKTIVTLFVLLVWLFIREP
rNaDC3 300 GGMWRGWRKKNSKLODVAEDKAKAVIQEEFONLGPLKFAEQAVFILECLFAILLFSRDP

rNaCT 340 GFMPGW-LSTAWIEGNTKHVTDATVAIFVAILLFIIVPSQPKPFNFSRQTEERKTPFYPP
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rNaDC3 360 KFIPGW-ASLEAP----GFVSDAVTGVAIVTILFFFFPSQKPSLKWWFDFKAPNSE---TE

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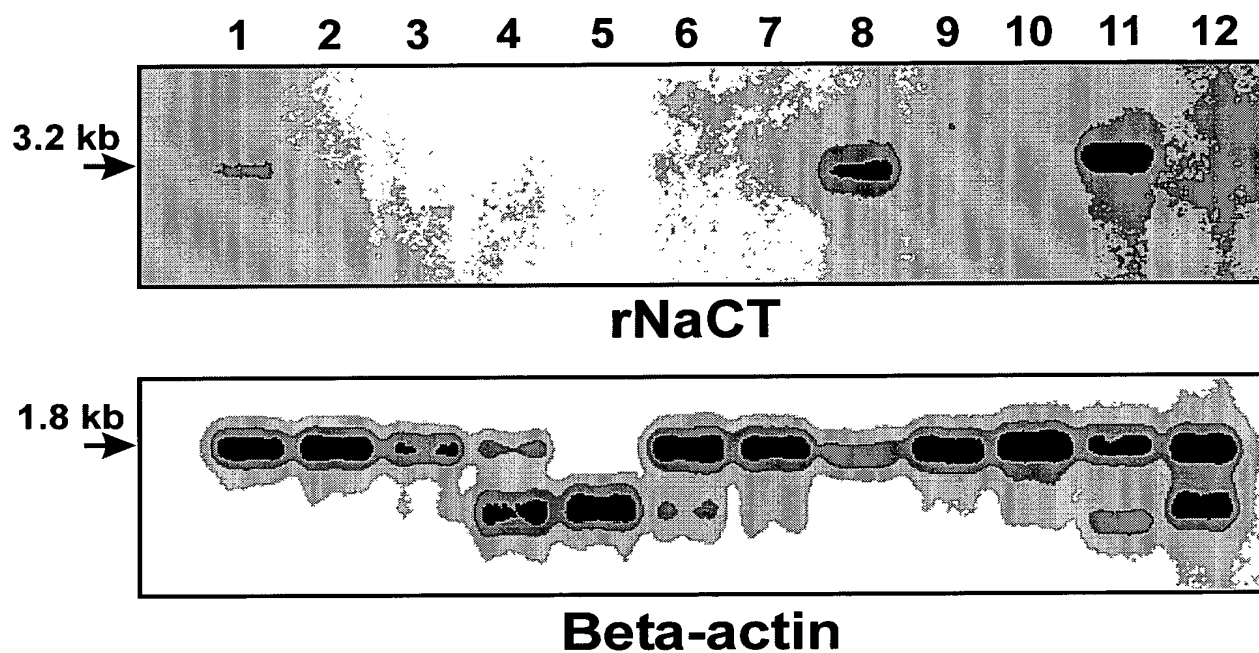
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rNaDC1 521 FSFGCLKVSDMARAGFLNIIIGVLATILSINSWSIPIFKLDTFPSWAHSNTSQCLLNP--
rNaDC3 532 FSTGHLLVKDMVRTGLLMNLMGVLLLSLAMNTWAQAIQOLGTFPDWANHAANVTALPPA

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rNaDC3 592 LTNNTVQTL-

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Fig. 9



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Fig. 10A

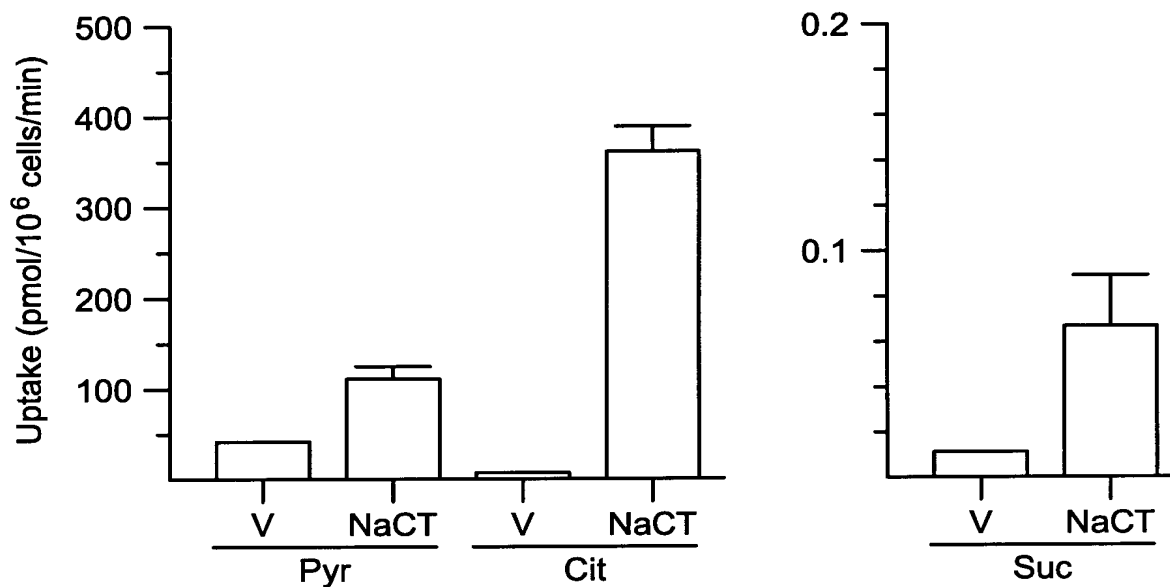


Fig. 10B

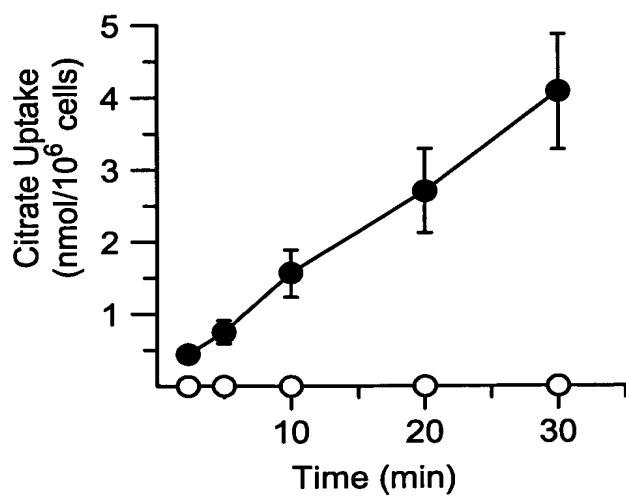
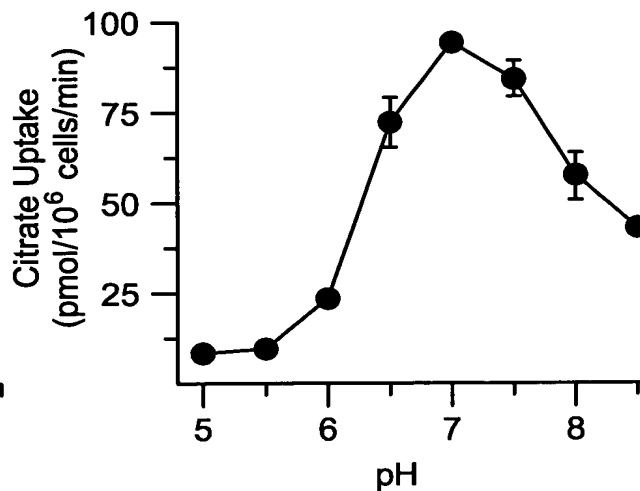


Fig. 10C



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Fig. 11A

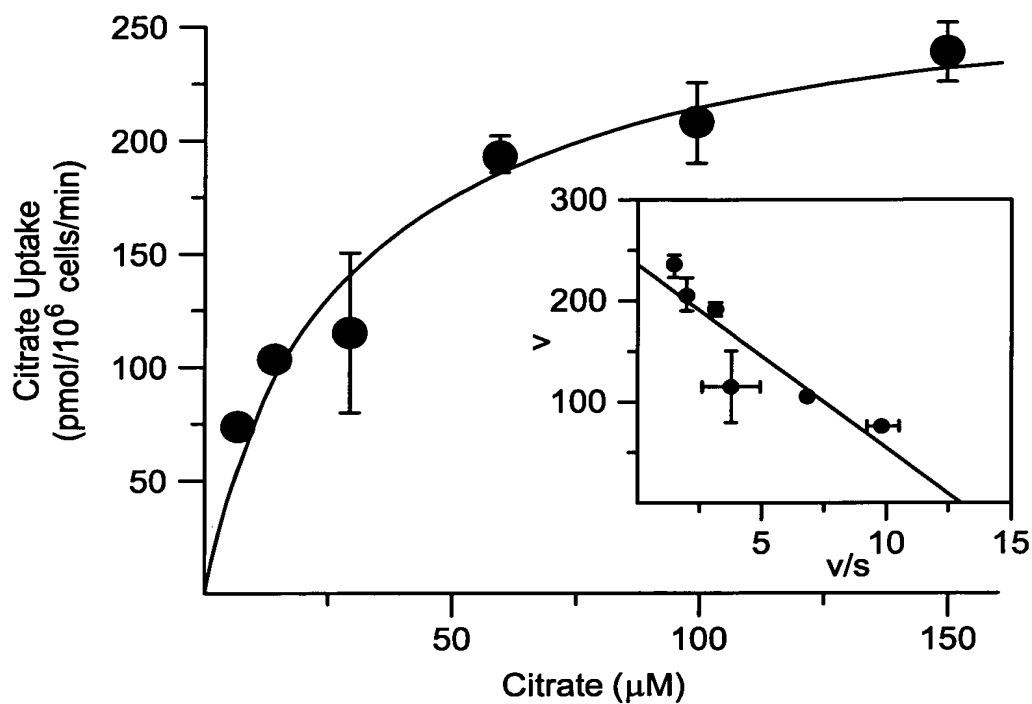


Fig. 11B

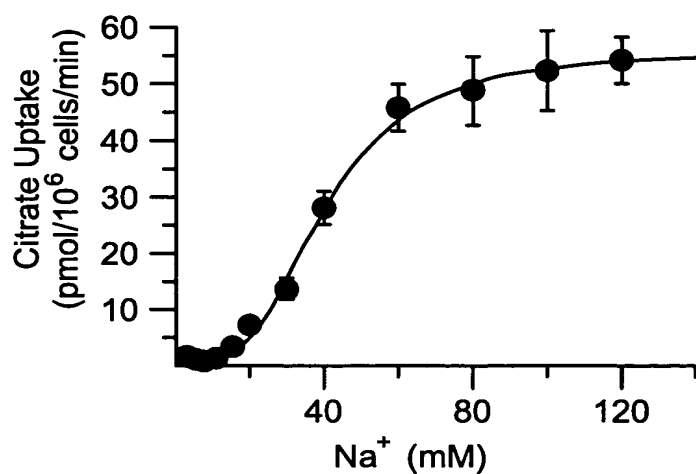
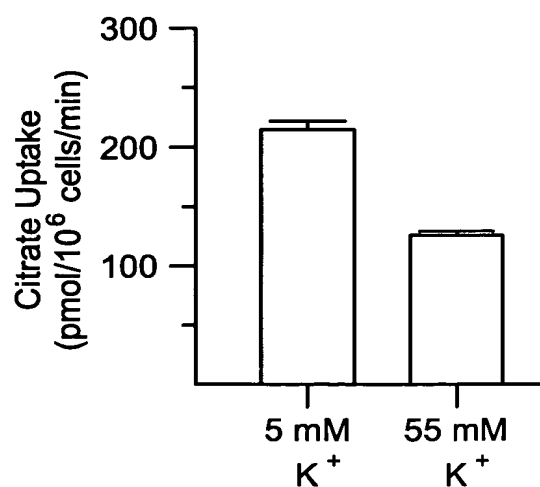


Fig. 11C



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Fig. 12A

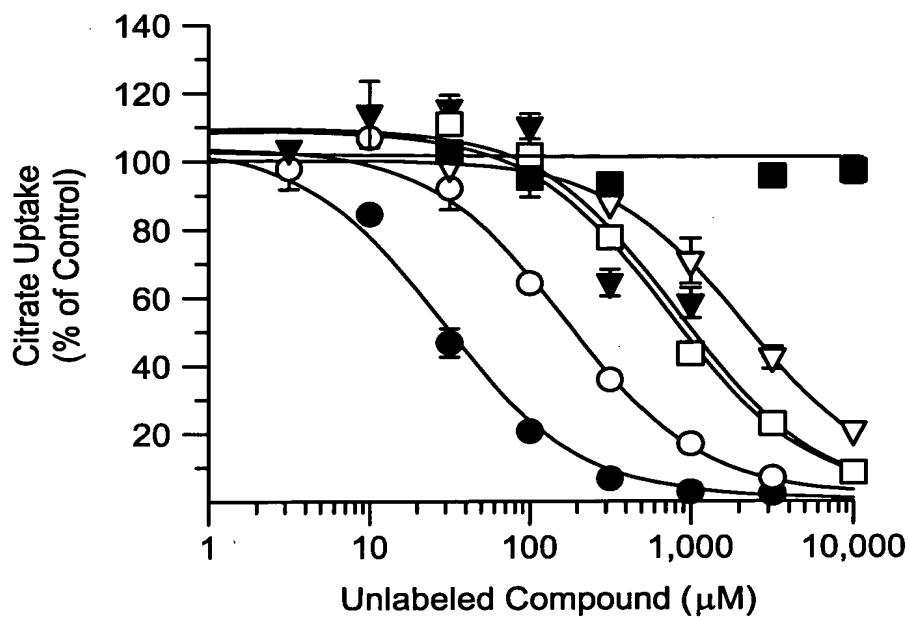
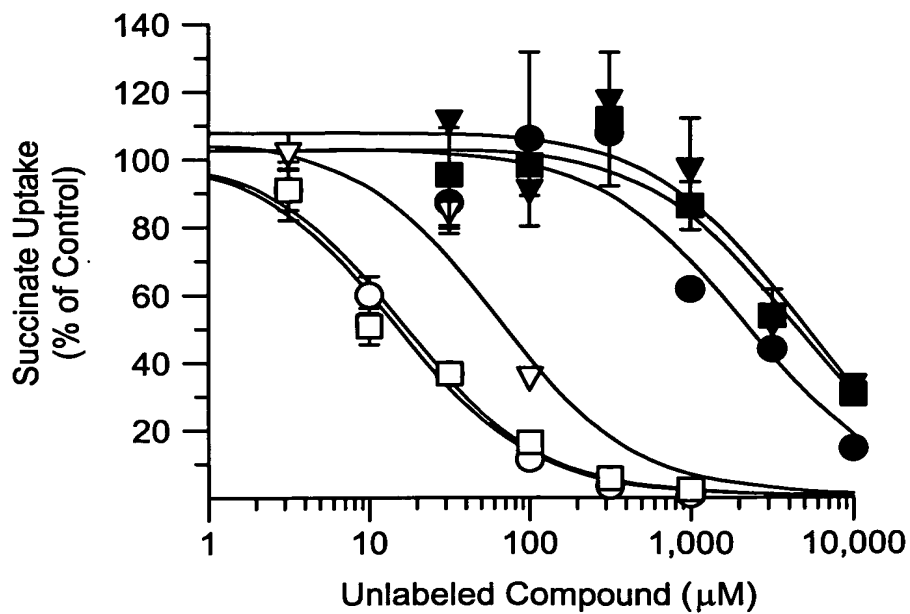


Fig. 12B



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Fig. 13A

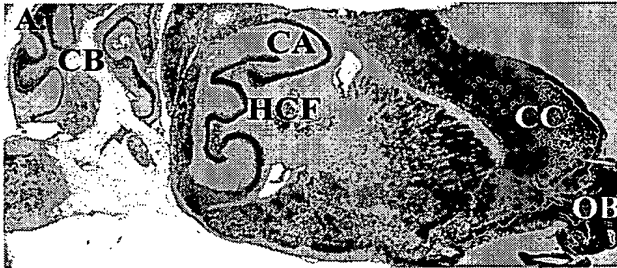


Fig. 13B



Fig. 13C

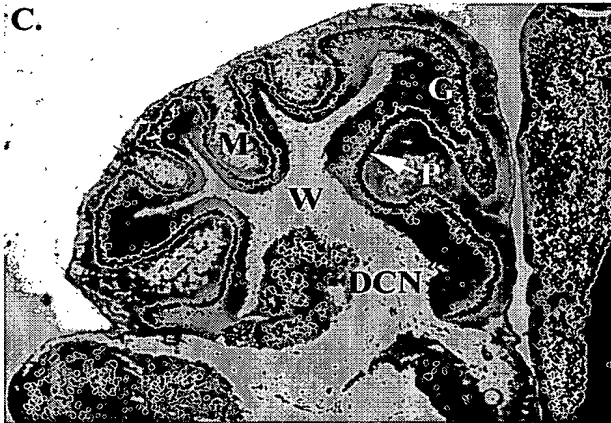


Fig. 13D

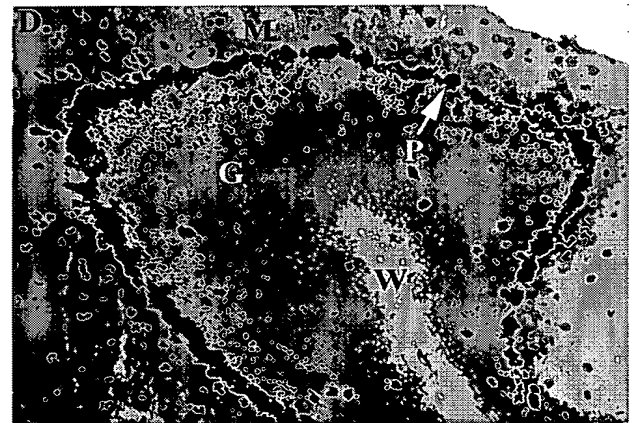


Fig. 13E

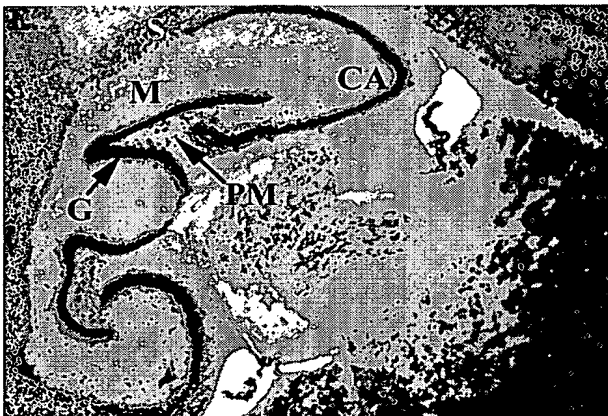


Fig. 13F

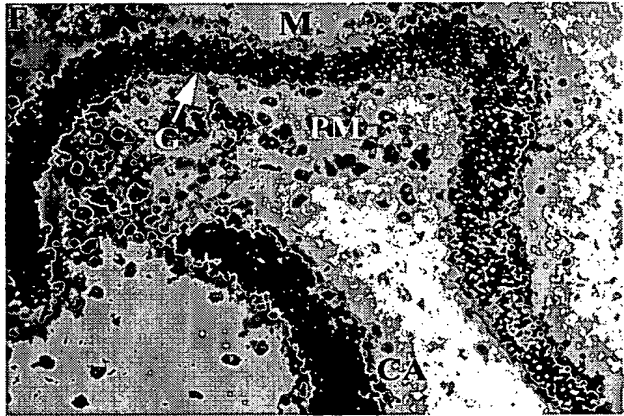


Fig. 14

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Human NaCT sequence
(3207 nt + 41 nt polyA)
ORF: 13-1719 (total 1707 nt)
SEQ ID NO: 5

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Amino acid sequence (568 aa)
SEQ ID NO: 6

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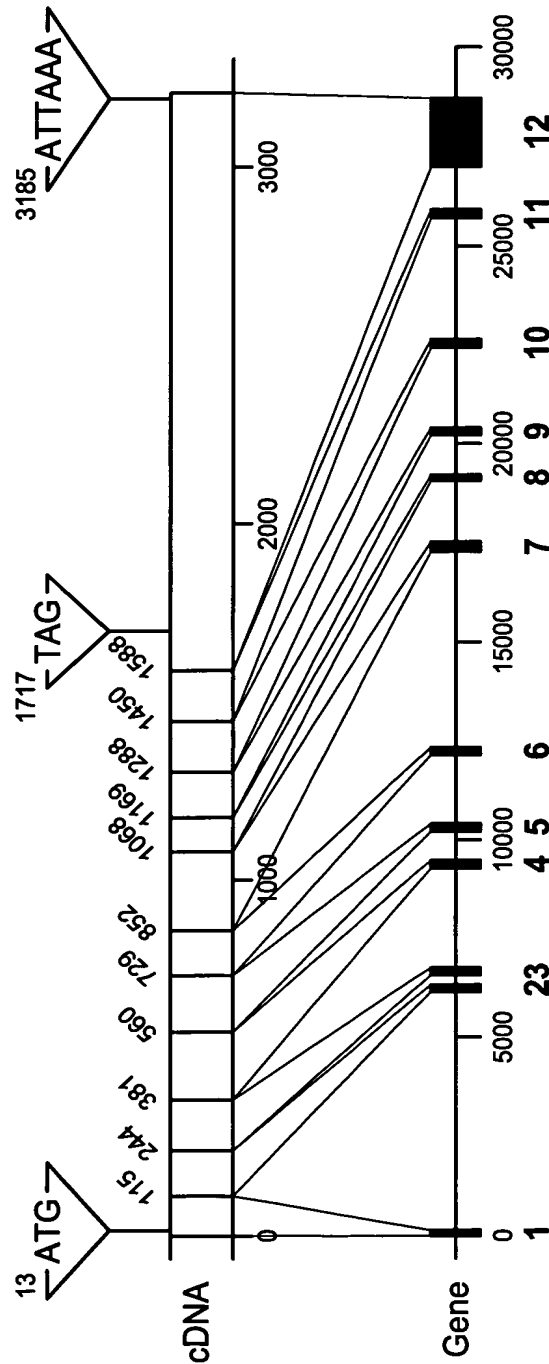
15/45

Fig. 15

human	1	MASALSYVSKFKSFVILFVTPILLLLPLVILMPAKFVRCAIVIIILMAIYWCTEVIPLAVTS
rat	1	MASAKTYVTKFKSFVILFAPILLLLPLIILVDPKFAKCAIVIIILMAIYWCTDVIPVAITS
human	61	LMPVLLFPLFQILDSRQVCVQYMKDTNMLFLGGLIVAVAVERWNLHKRIALRTLLWVGAK
rat	61	LLPVLLFPLLKVLDSKQVCVQYMTDTNMLFLGSLIVATAVERWELHKRIALRMILLEVGTK
human	121	PARLMLGFMGVTAFLSMWISNTATTAMMVPIVEATLQOMEATSAATEAG---LELVDKCK
rat	121	PSRLMLGFMFVTAFLSMWISNTATTAMMIPIVEAMLEQMVATNVAVDASQRTMELLDDKNK
human	178	AKELPGSQVIFECPTLGOQEDQERKRLCKAMTLCICYAASIGGTATLTGTGPNVVLLGQM
rat	181	ASELPGSQVVFEDPSVQKQEDDEETKNMYKAMNLCVCYAASIGGTATLTGTGPNVVLLGQM
human	238	NELFPDSKDLVNFASWFAFAPNMLVMLLEAWLWLQFVYMRPNEFKKSWGCGLESKK-NEK
rat	241	QELFPDSKDVNFASWFAFAPNMLLLMLVMAWLWLLCFYMRPNKKTCICCGRKKKDKTEK
human	297	AALKVLQEEYRKLGPLSFAEINVLICFFLLVILWFSRDPGFMPGWLTVAVVEGETKYVSD
rat	301	IASKVLVEEYRKLGPLSYAECNVLFCEGLLLILWFSRDPGFMPGWLSIAWIEGNTKKHVID
human	357	ATVAIFVATLLFIVPSQKPKFNFRSQTEERKTPFYPPPLLDWKVTQEKVPWGIVLLGG
rat	361	ATVAIFVAIILLFIVPSQKPKFNFRSQTEERKTPFYPPPLLNWKVTQEKVPWGIVLLGG
human	417	GFALAKGSEASGLSVWMGKQMEPLHAVPPAAITLILSLIVAVFTECTSNVATTTFLFLPIF
rat	421	GFAMAKGCETSGLSEWMARQMEPLSSVRPAITLILSCIVAMTTECTSNVATTTFLFLPIF
human	477	ASMSRSIGLNPLYIMLPCTLSASAFMLPVATPPNAIVFYGHLKVADMVKTGVEMNIIG
rat	481	ASMARSIGIIEPLYVMIPCTLSASAFMLPVATPPNAIVFAYGHLKVIDMVKTGLVMNIIIG
human	537	VFCVFLAVNTWGRAIFDLDHFPDWANVTHIET
rat	541	IASVFLSVNTWGRAVENLDKFPDWANLTHINT

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Fig. 16



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Fig. 17A

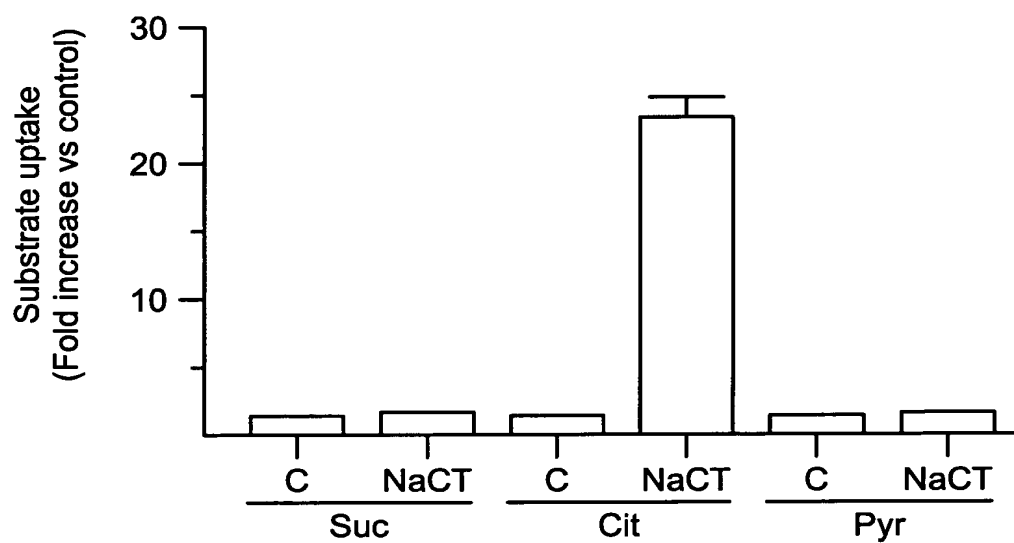
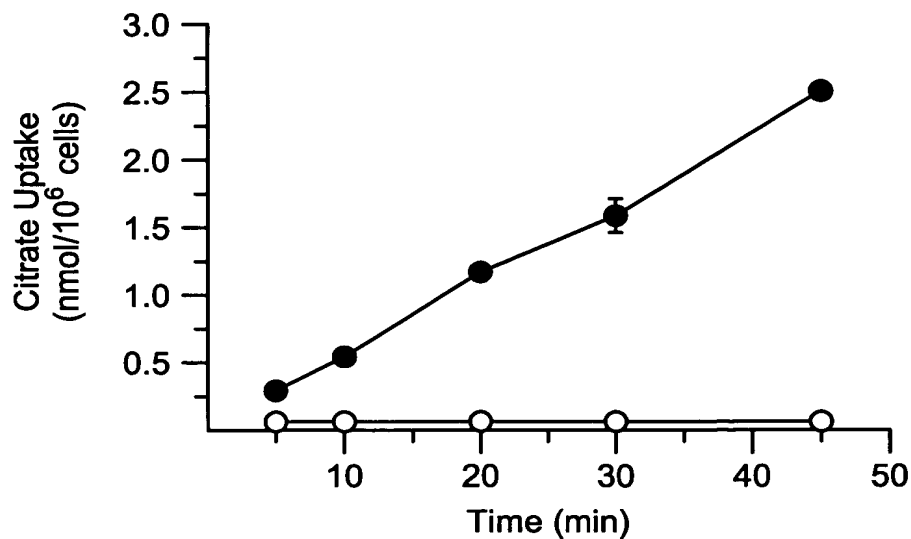


Fig. 17B



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Fig. 18A

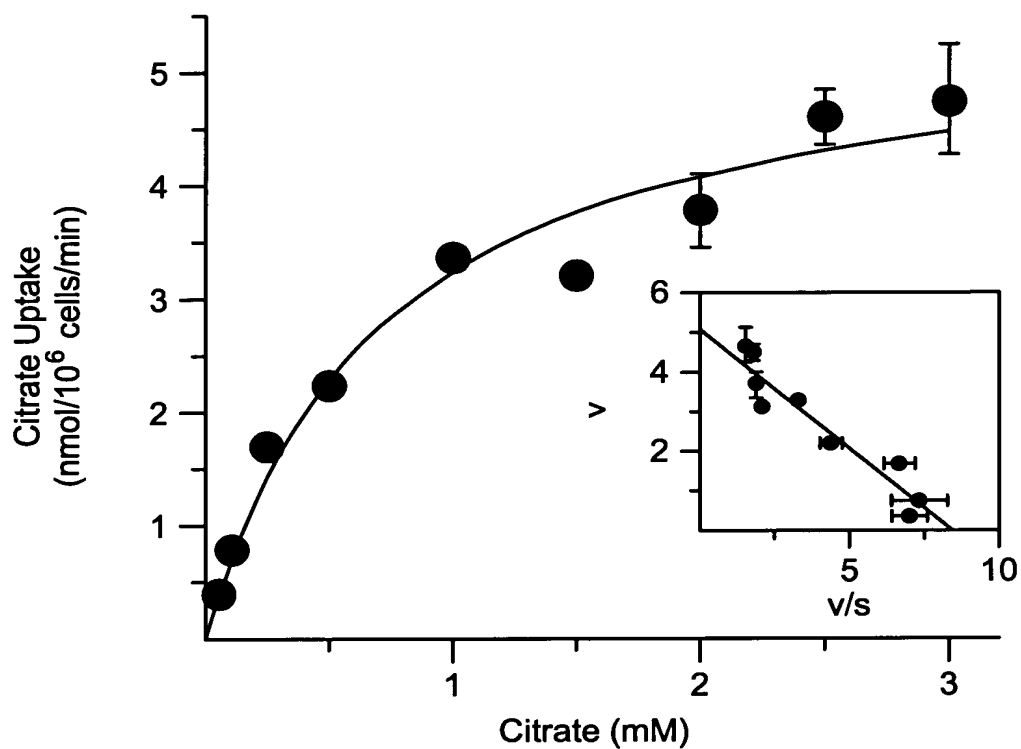
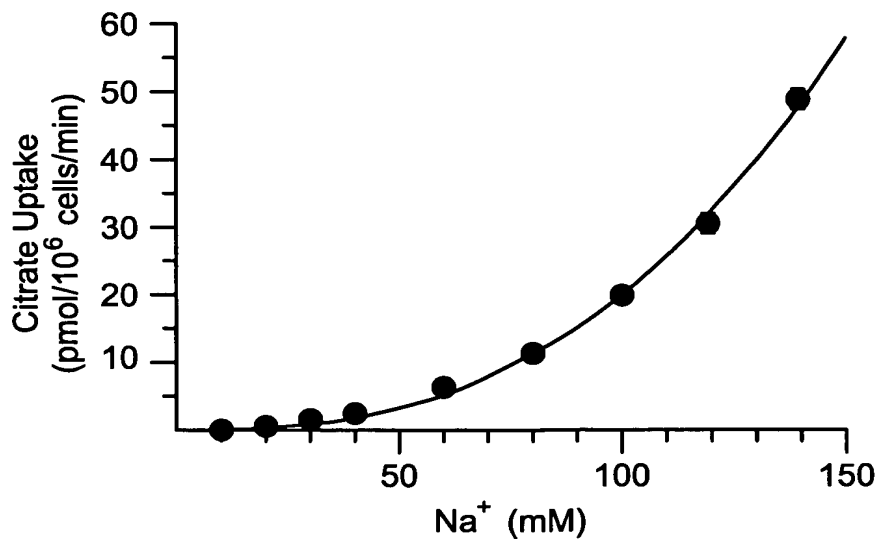


Fig. 18B



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ceNaCT cDNA & Protein Sequences

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101	200	CTCTACTCTTTTTGGACCGGAGTACAGATGCTTTTCTCAATAATATTTTATCAACCTATTGGATTGGAGAAGCATTTCCCATTTGGTGTCACTTCTCT
201	300	CTTTCCATTGGCACCTTTATCCAAATCTTCAGATTGTCCATCTAAACAATAATAGTCCAGTTTATTTAAAGATTCGATAGTTCATTTATGTGCACATTA
301	400	AGCATGGCAATGGCGGTGAAGCAACTGGACTCCATCGAAGAATCGCACTGAAATATTAAACAAAAGTTGGAGCAAAAGCAACCAGTAATGCTGGGTT
401	500	TCATGTGCATCAGAGTTTCATATCATTTTTTCGTTTCTGACACAGCATGCACAGCTCTTATGTGTCCAACCGCTGTGGCACTCCTGATGAGTATGTCGTA
501	600	TGCAGTTCAACATTTGAAAGAAGATCAGAGGAAGCCAAAGCCGCCACAGATGATGCTACTGTTGCTGAAAAAATGAGAATAGATGATGACTCCTCAG
601	700	GATGCTGGTTTCTGTAAGCATTAATTTTGGCATGTGCCACGCATCGTTGATCGGTGGACTGCTATTATCACTTCGACTGGCGCAATTAGTTTTTC
701	800	DAGFCCKALILACAHASLIGGTALIIITSTGPNLVFR
801	900	ATCTTATATTCTGGTGTATTATTCATGGGCCCTCGACTTTTGTCTGCTGGTTGAAAGGCCTTCCAAGAAGAAGCTCATTTGAAAAAATAATT
901	1000	SYIILVCFMGPSTFARWFE RPSKEEAHLKKL
1001	1100	CTCGTATCCCGGATTCACACCCGGTTGGGAGATCTTTTACCACACAGAAACCTCATATCAGACAGTGTTCGAGTCTTGATTTCTTGATTTTATT
1101	1200	TGTTGGCCCCAAGATCCATTGATCCTATTGATCCAATGGCTCCGATTCTTAATGACCGACATGAAAGCAAGTTTCTGGTCGTGCACACTTTTA
1201	1300	ATCGTGTGGGTATGCTATTTCAGAAAGGATTGATAAATCGGGATTATCTAGATTGATTTATGATTTTCTGAGTCTTGATTTCTTGATTTTATT

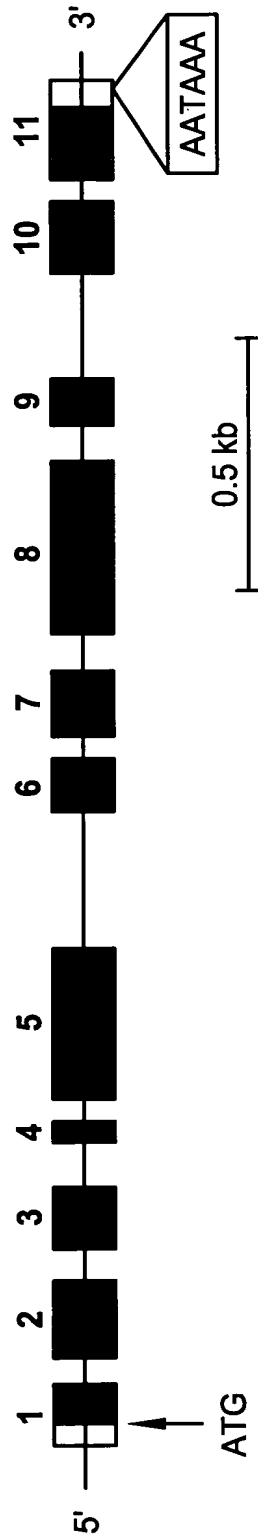
20/45

Fig. 19B

1301	TTCCATTGCAATTAACTGTGACTACAAATTATTGTGATAAATGACAGAGTTTGCAGTAATGTGTCCACCGGAAGCATTTCATTCCCAATTTCTTTGGGAGT	1400
	P L Q L T V T I I V I I M T E F A S N V S T G S I F I P I S L G V	
1401	TGCTGAATCAATGGGAGTTCATCCTTTATATCTTGCTCTTCCAACTACTGTAGCTTGTTTCATTGCTTTTATGCTACCAATTTCAACACCTCCAAATGCA	1500
	A E S M G V H P L Y L A L P T T V A C S F A F M L P I S T P P N A	
1501	GTTGTATACGACACTAAAGTGATTTCAATGGTGGAAATGATAGTCTGTGGTTTTCTACTCAATATTGCGTGCATACCTATCACATCTCTCAACATGAACA	1600
	V V Y D T K V I S M V E M I V C G F L L N I A C I L I T S L N M N T	
1601	CATGGACATATTTTATTTTTCATTGAATATTTTCCCGGAAATATTGTAATATCTTCAGAAAACCTCTTCATATCCAGTTGCTAATTTTGTACAAAAT	1700
	W T Y F I F I S L N I F P E N I V I S S E N S S Y P V C *	
1701	GTGTATTGTCGGAATGAAACGTGTATTATTATAAAAAAAAAAAAAA	
	-----+----- 1747	

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Fig. 20



REPLACEMENT SHEET

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Fig. 21

1	drIndy	M	E	I	E	G	E	Q	P	Q	60	M	Y	L	L	V	M	A	I	E			
	ratNaCT	~	~	~	~	~	~	~	~	~	120	A	Y	V	I	I	L	M	A	I	Y		
	ceNaCT	~	~	~	~	~	~	~	~	~	180	L	F	S	I	I	F	S	T	Y			
61		W	V	T	E	A	L	P	L	Y	V	220	A	V	E	Y	C	N	L	H	K	R	
	W	C	T	D	V	I	P	V	A	I		240	A	V	E	R	W	E	L	H	K	R	
	W	I	G	E	A	F	P	I	G	V		260	A	V	E	A	T	G	L	H	K	R	
121		I	A	L	R	M	L	L	T	K	V	300	L	Q	A	Q	G	V	C	~	~	~	
	I	A	L	K	L	L	T	K	V	G		320	M	V	A	T	N	V	A	V	D	A	
181		~	~	~	~	~	~	~	~	~	~	340	M	~	~	~	~	~	~	~	~	~	
	S	Q	R	T	M	E	L	L	D	K		360	S	S	L	G	G	C	G	T	I	I	
	V	Q	H	L	K	E	~	~	~	~	~	380	A	S	I	G	G	T	A	T	L	T	
241		G	T	A	T	N	L	T	F	K	G	400	F	M	G	L	N	R	P	P	K	S	K
	G	T	C	P	N	V	V	L	L	G		420	Y	M	~	~	~	~	~	~	~	~	
	S	T	G	P	N	L	V	F	R	E		440	F	M	G	~	~	~	~	~	~	~	
301		E	A	Q	E	V	Q	R	G	R	E	460	F	T	R	K	P	G	I	F	L	G	
	K	T	C	~	I	C	C	G	R	K		480	F	S	R	D	P	G	F	M	P	G	
	A	R	W	F	E	R	P	S	K	E		500	I	S	R	D	P	G	F	T	P	G	
361		W	A	D	L	~	~	~	~	~	~	520	P	T	G	P	T	P	S	L	I	T	
	W	L	S	I	A	W	I	E	G	N		540	P	P	F	Y	P	~	~	~	~	~	
	W	G	D	L	~	~	~	~	~	~	~	560	P	I	D	P	M	A	P	I	L	K	
421		W	K	F	I	Q	T	K	V	P	W	580	L	L	L	V	V	I	L	V	A	V	
	W	K	V	T	Q	E	K	V	P	W		600	L	T	L	I	L	S	C	I	V	A	
	W	T	D	M	K	S	K	F	S	W		620	L	Q	L	T	V	T	I	I	V		
481		F	L	T	A	F	S	S	N	V	A	640	T	P	P	N	A	L	V	A	G	Y	
	M	T	T	E	C	T	S	N	V	A		660	T	P	P	N	A	I	V	F	A	Y	
	I	M	T	E	F	A	S	N	V	S		680	T	P	P	N	A	V	V	Y	D	T	
541		A	N	I	R	T	K	K	D	M	A	I	700	A	A	L	G	N	K	T	H	~	
	G	H	L	K	V	I	D	M	V	K		720	N	T	~	~	~	~	~	~	~	~	
	K	V	I	S	M	V	E	M	I	V		740	N	S	S	Y	P	V	C	~	~	~	

Fig. 22A

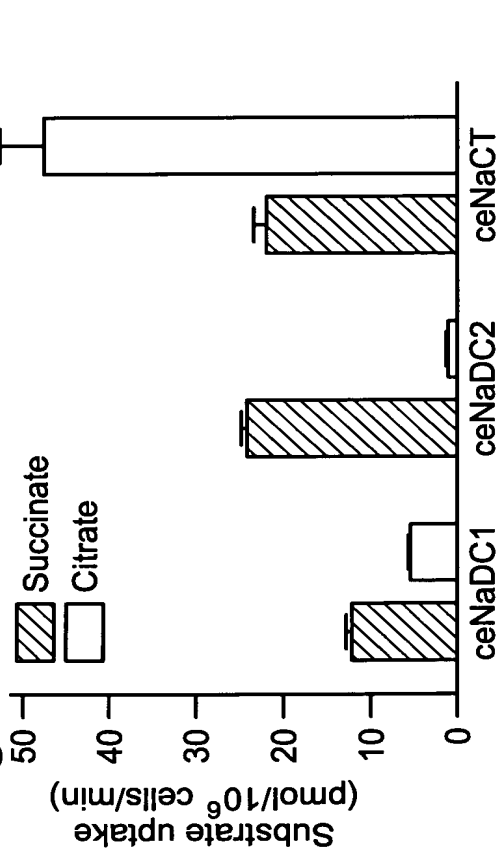


Fig. 22B

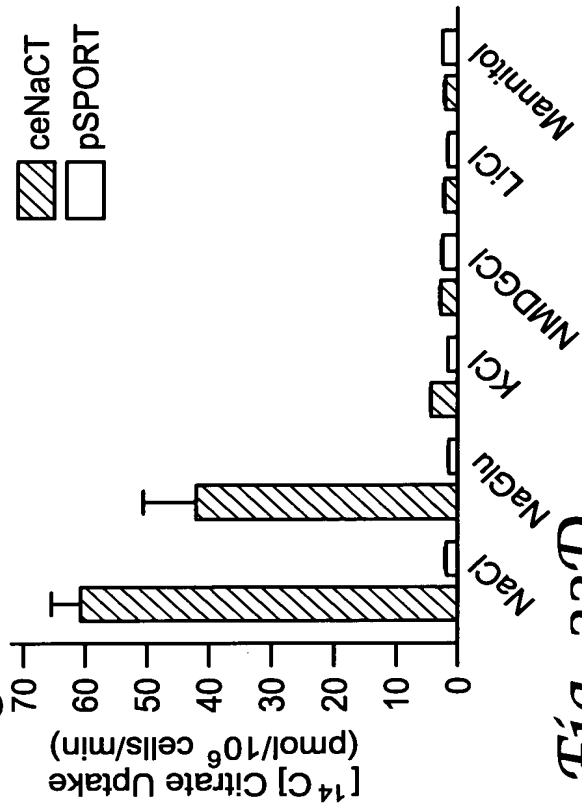


Fig. 22C

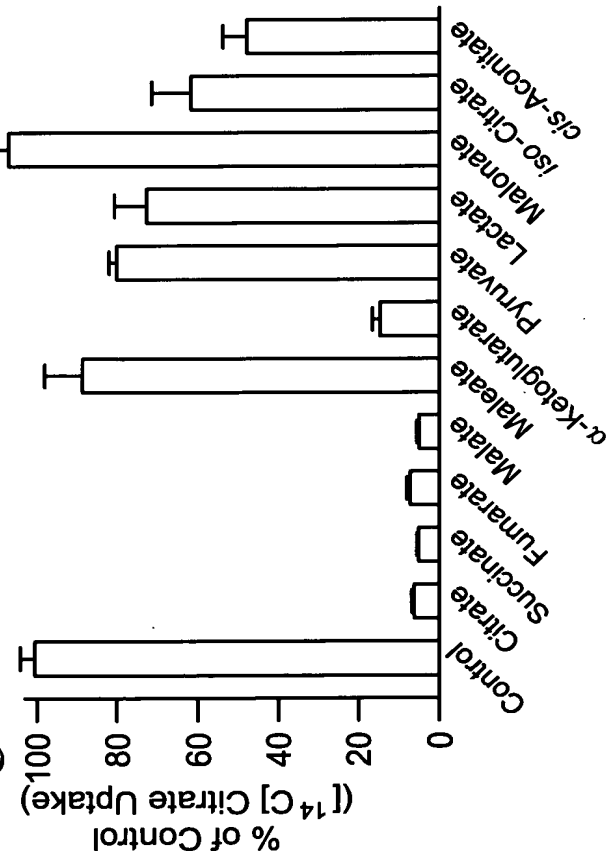
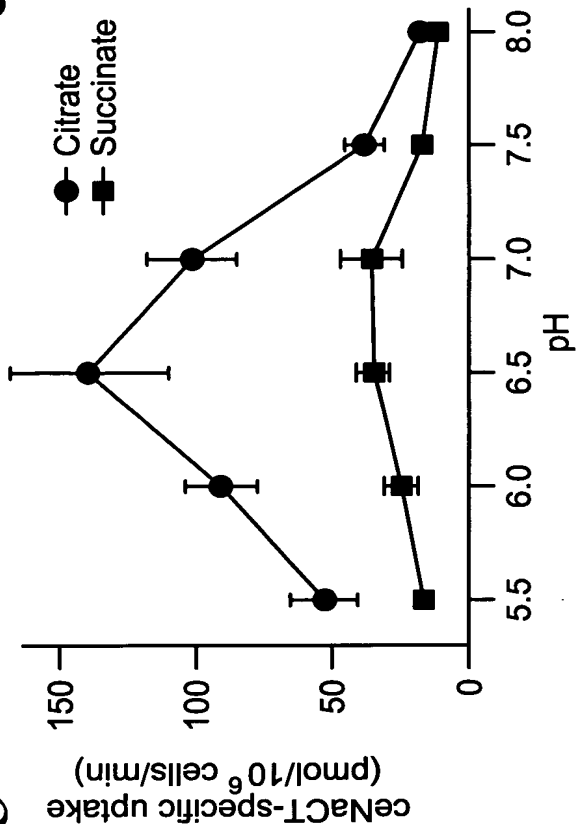


Fig. 22D



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Fig. 23A

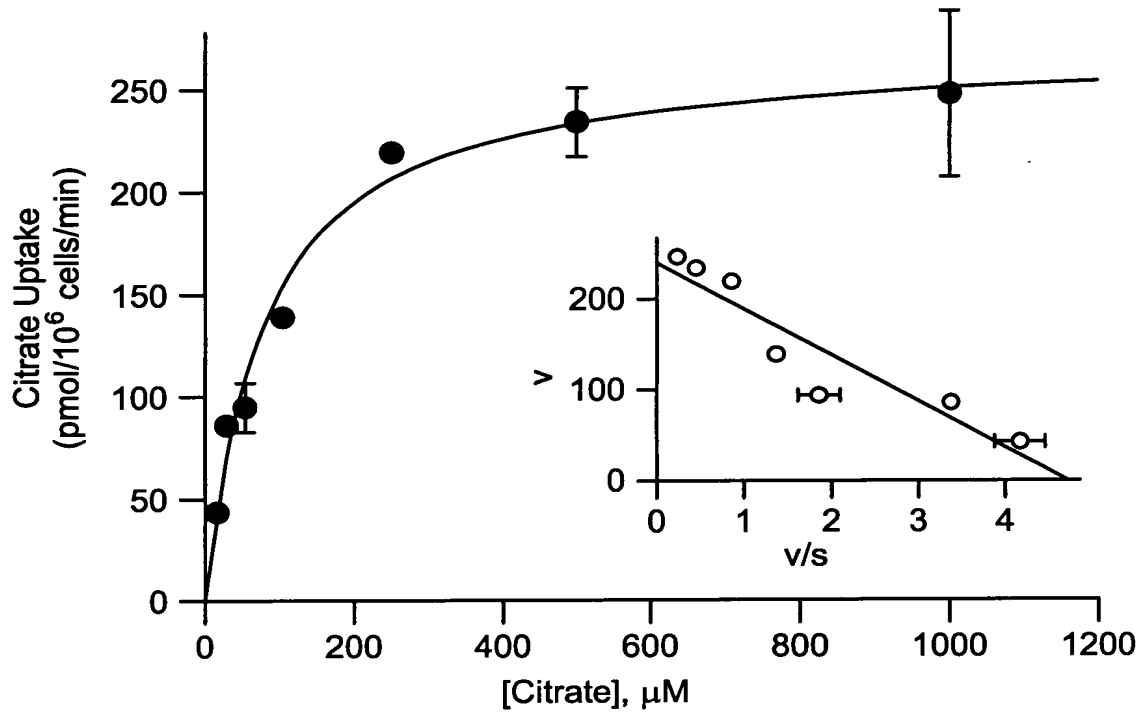
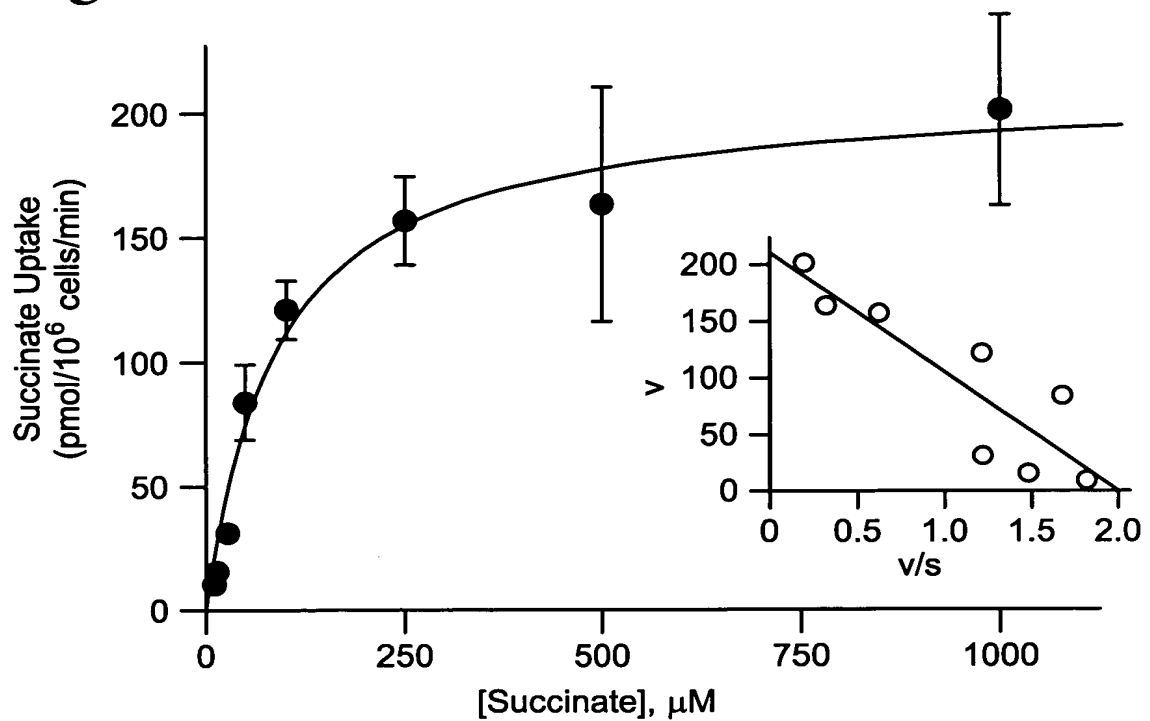


Fig. 23B



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Fig. 24B

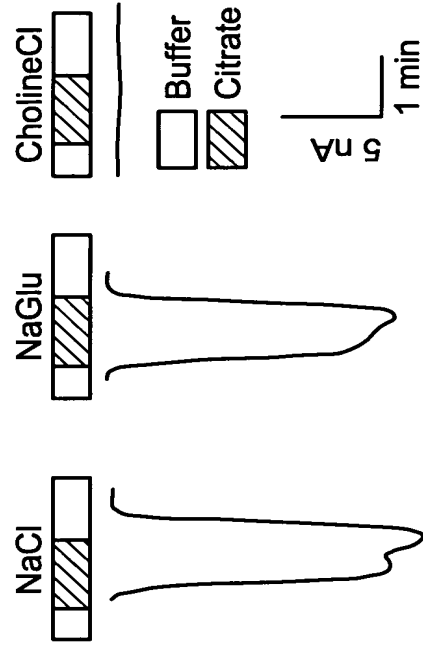


Fig. 24A

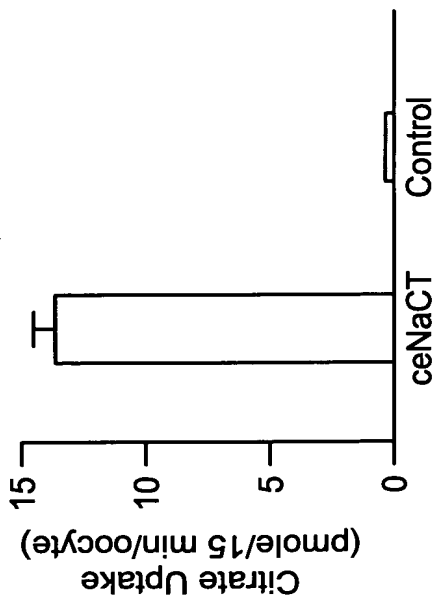


Fig. 24D

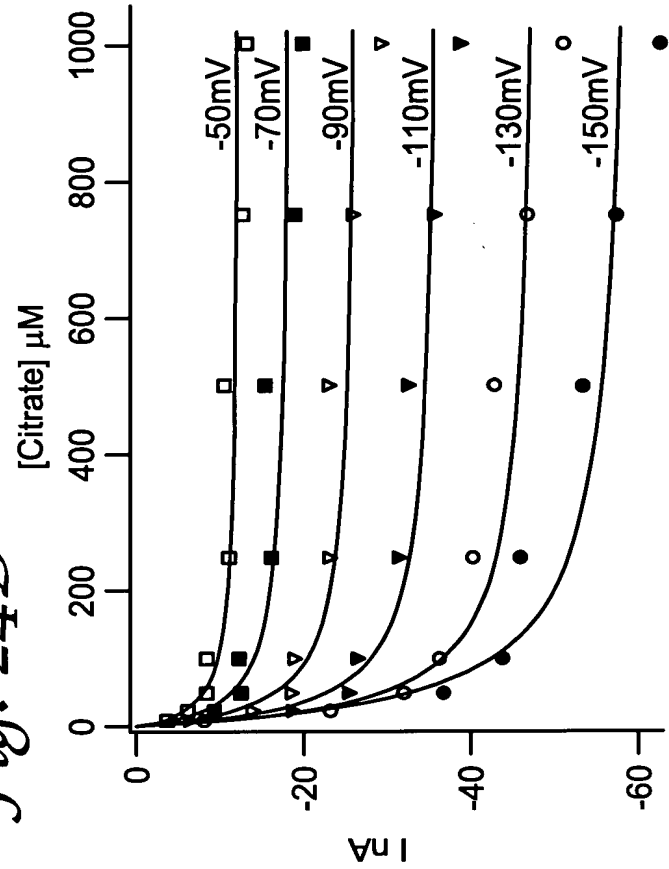
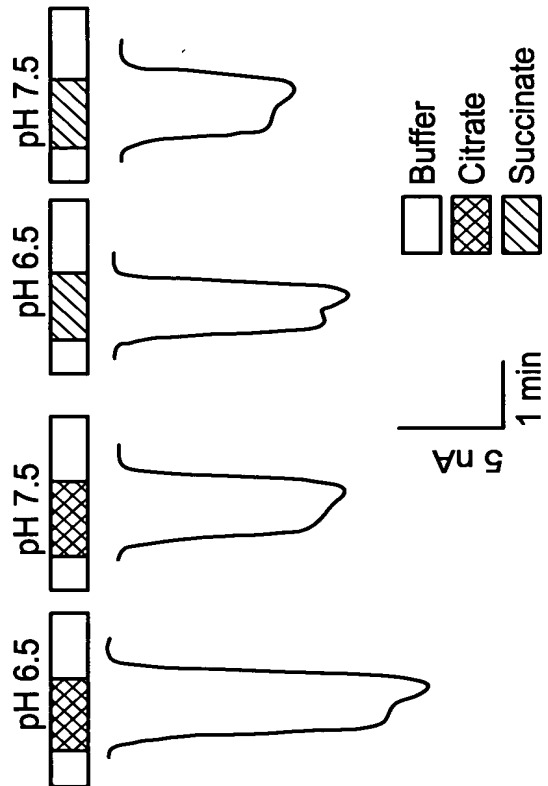


Fig. 24C



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Fig. 25A

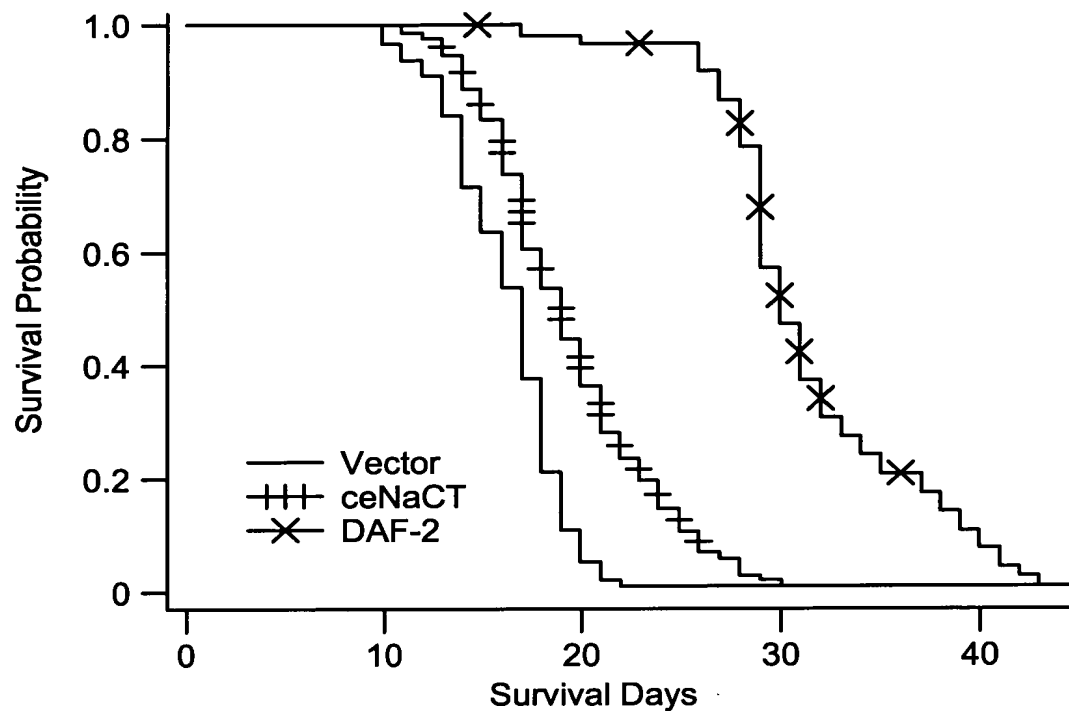
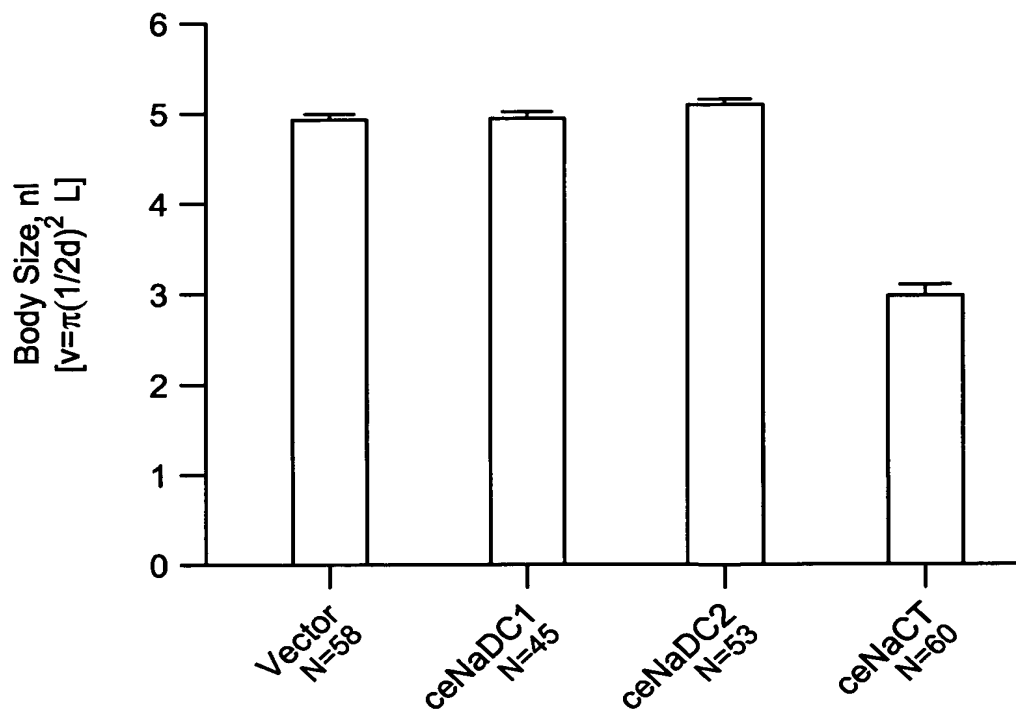


Fig. 25B



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Fig. 26

RNAi; ceNaCT & pPD129; Nile Red (0.05 µg/ml) staining

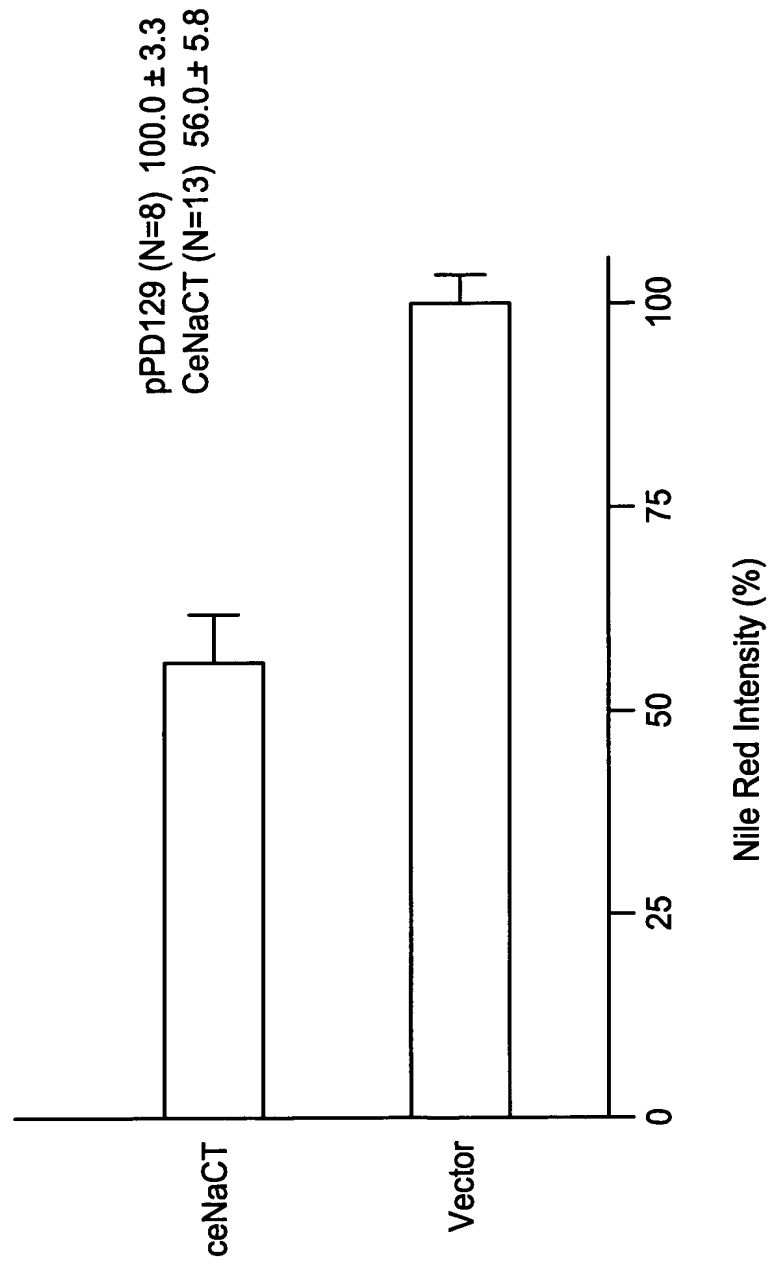


Fig. 27

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Mouse NaCT sequence
cDNA sequence (16 nt + 1719 nt)
SEQ ID NO: 9

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Protein sequence (572 nt)
SEQ ID NO: 10

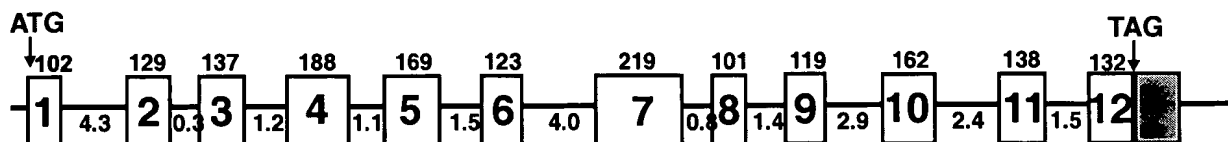
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Fig. 28A

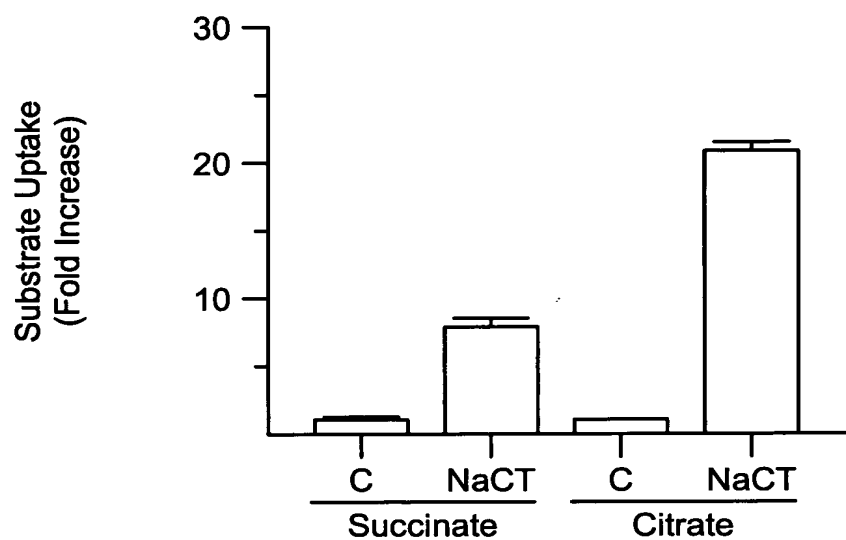
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rat	1	MASAKTYVTKFKSFVILFFAPILLPLLLILVDPDKFARCAIVILMAIYWCTDVIPVAVTS
human	1	MASALSIVSKFKSFVILFVTPLLLLPLVILMPAKFVRCAYVILMAIYWCTEVIPIAVTS
mouse	61	LLPVLLFPLLKVLDISKQVCIQYMKDNTNMLFLGSLIVAVAVERWKLHKRVALRMLLFFVGTK
rat	61	LLPVLLFPLLKVLDISKQVCVQYMTDNTNMLFLGSLIVATAVERWELHKRIALRMLLFFVGTK
human	61	LMPVLLFPLLFQILDSRQVCVQYMKDNTNMLFLGCLIVAVAVERWNLHKRIALRMLLWVCAK
mouse	121	PSRLMLGFMFVTAFLSMWISNTAATAMMIPIVEAMLOQMIAANTAVEASLGTTLELLDKNK
rat	121	PSRLMLGFMFVTAFLSMWISNTATTAMMIPIVEAMLEQMVA TNVAVDASQRTMELLDKNK
human	121	PARLMLGFMGVTAFLSMWISNTATTAMMIPIVEAILQOMEATSAATEAG---LELVDKCK
mouse	181	TSELPGSQVVFEDPNVQEQEDEETKNMYKAMLCVCYASISIGGTATLTGTGPNVLLGQM
rat	181	ASELPGSQVVFEDPSVQKQEDEETKNMYKAMLCVCYASISIGGTATLTGTGPNVLLGQM
human	178	AKELPGSQVVFECPTLGOQEDQERKRLCKAMLCICYASISIGGTATLTGTGPNVLLGQM
mouse	241	QELFPDSKDVLNFAWFGFAFPNMVMLVLAWLWLOCLYMRNLKKTICCCGEKKRDTEK
rat	241	QELFPDSKDVLNFAWFAFALPNMLMLVMAWLWLCLFYMRNLKKTICCCGRKKKRDTEK
human	238	NELFPDSKDVLNFAWFAFAPNMLVMLLFAWLWLOFVYMRNLKKSWSGCGLESKK-NEK
mouse	301	IAYKVLNEEYQKLGSLSYPECNVLFCEFLLVILWFSRDPGFMPGWLSFAWVEGNTVHETD
rat	301	IASKVLYEEYRKLGPLSYAECNVLFCEFLLVILWFSRDPGFMPGWLSFAWTEGNTKHVTD
human	297	AALKVLQEEYRKLGPLSFAETNVLICFFLLVILWFSRDPGFMPGWLTVAWVEGETKYVSD
mouse	361	ATVAIFVAILLFIIIPSQKPKFNFSQTEERKTPFYPPALLDWKVAQEKVPWDIVLLLG
rat	361	ATVAIFVAILLFIVPSQKPKFNFSQTEERKTPFYPPPLLNWKVTQEKVPWGIVLLLG
human	357	ATVAIFVATLLFIVPSQKPKFNFSQTEERKTPFYPPPLLDWKVTQEKVPWGIVLLLG
mouse	421	GFAMAKGCETSGLSKWMARQMEPLRLVKPAVITLILSCLVAMTTECTSNVATTTFLFPIF
rat	421	GFAMAKGCETSGLSKWMARQMEPLSSVRPAVITLILSCLVAMTTECTSNVATTTFLFPIF
human	417	GFALAKGSEASGLSVWMGKQMEPLHVPAPAVITLILSLVAVTECTSNVATTTFLFPIF
mouse	481	ASMARSIGIHPLYVMIPCTMSASLAFMLPVATPPNAIVFAYGHLRVVDMMKTGIMNFVG
rat	481	ASMARSIGIHPLYVMIPCTLSASLAFMLPVATPPNAIVFAYGHLKVIDMVKTGLVMNLLG
human	477	ASMSRSIGLNPLYTMLPCTLSASTAFMLPVATPPNAIVFTYGHKLVADMVKTGVIMNLLG
mouse	541	ILSVFLSVNTWGRAMFNLDNFDPDWANSTSVNT
rat	541	IASVFLSVNTWGRAVFNLDFPDWANLTHINT
human	537	VFCVFLAVNTWGRAIFDLDFPDWANVTHIET

Fig. 28B



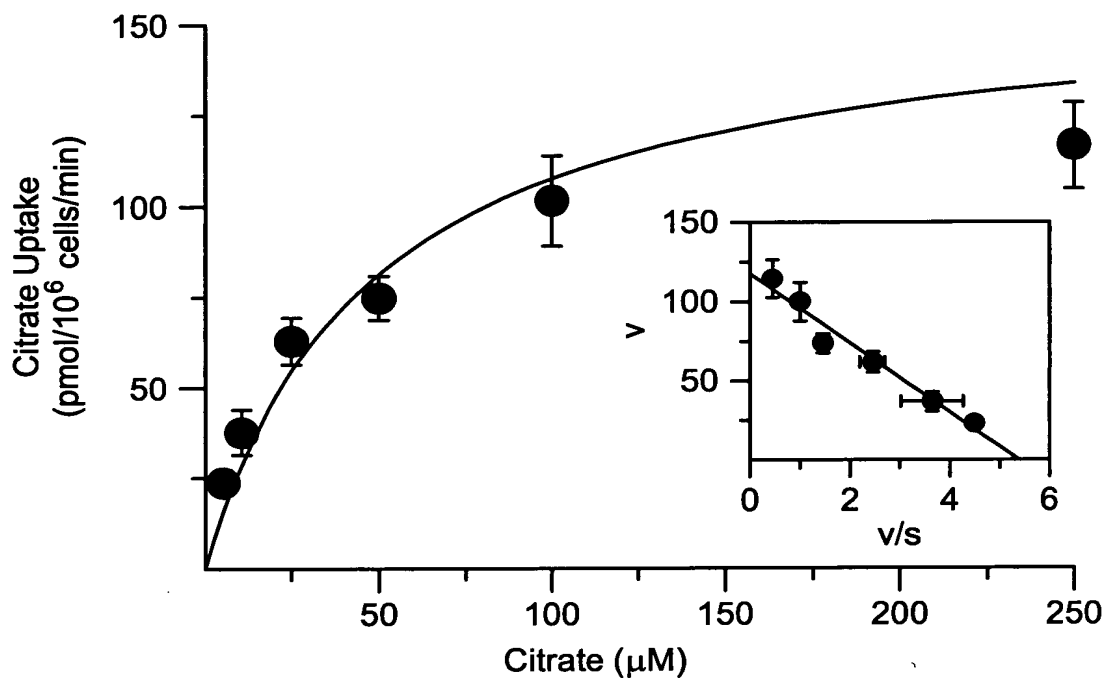
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Fig. 29



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Fig. 30A



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Fig. 31A

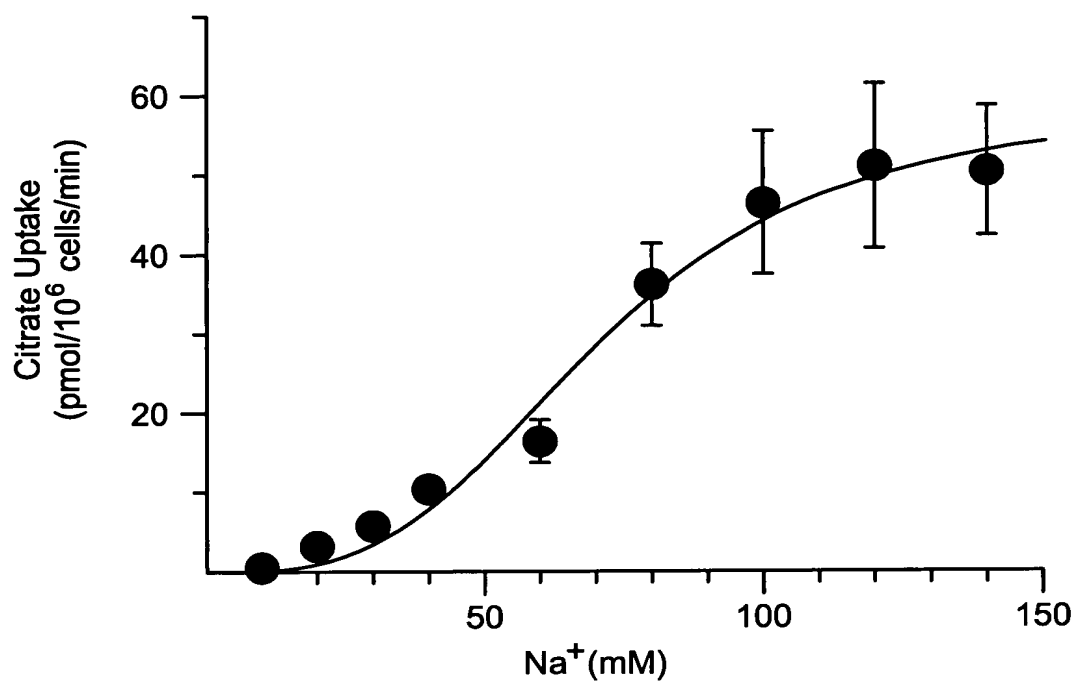
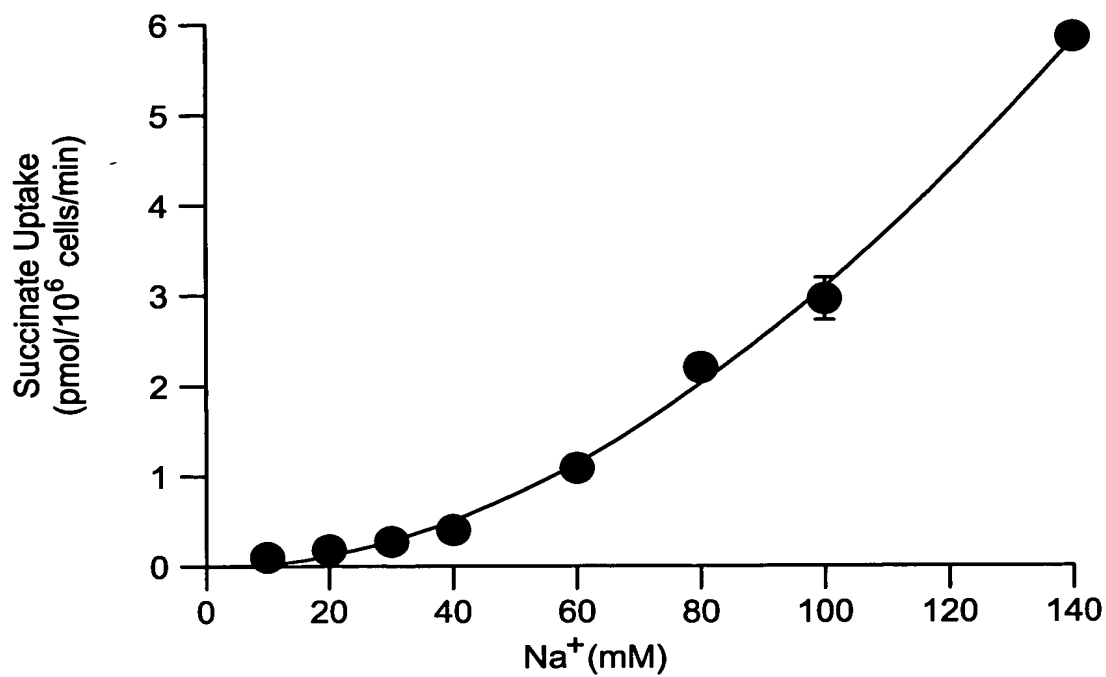
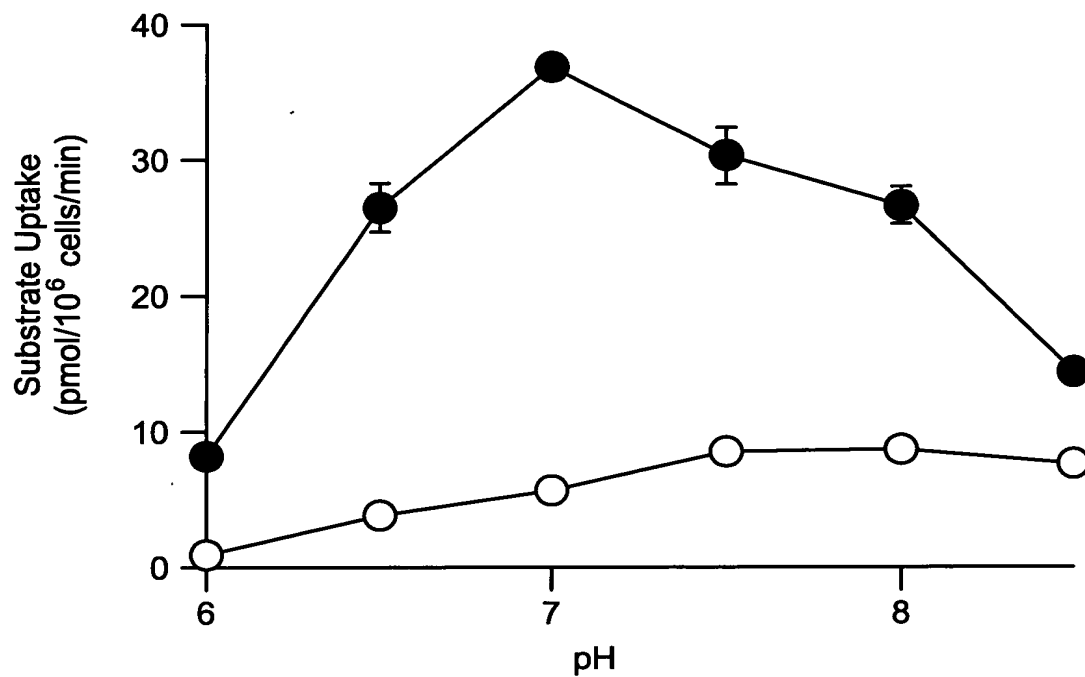


Fig. 31B



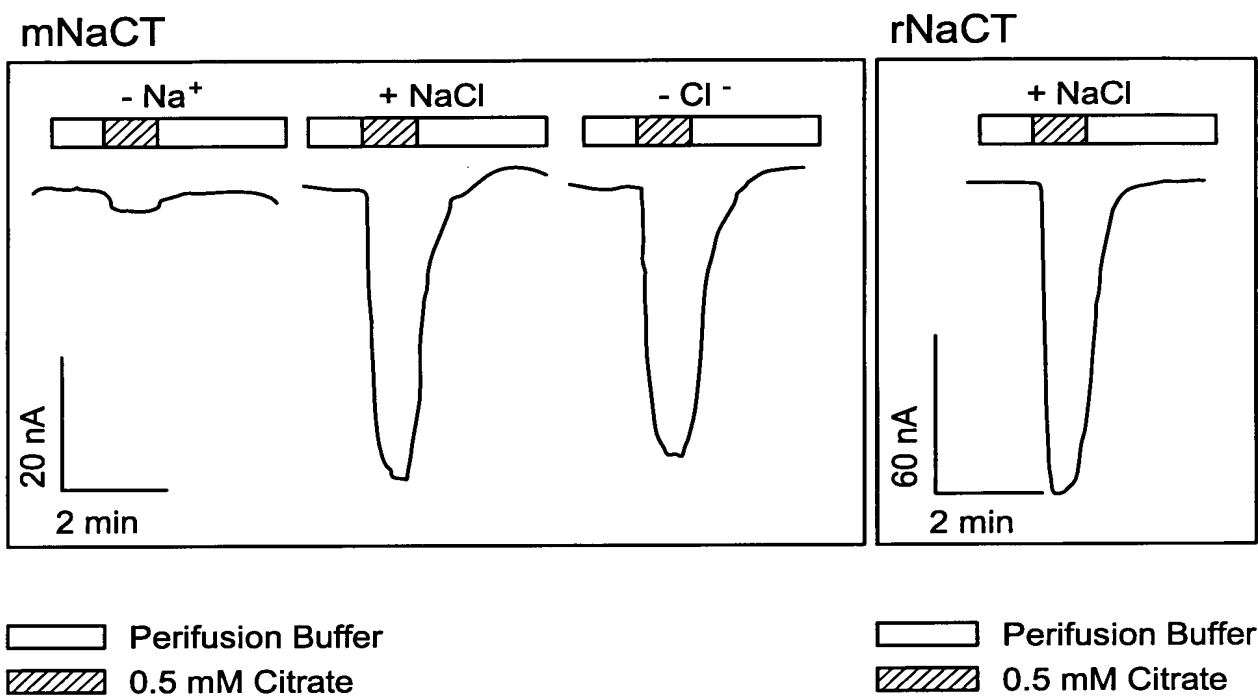
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Fig. 32



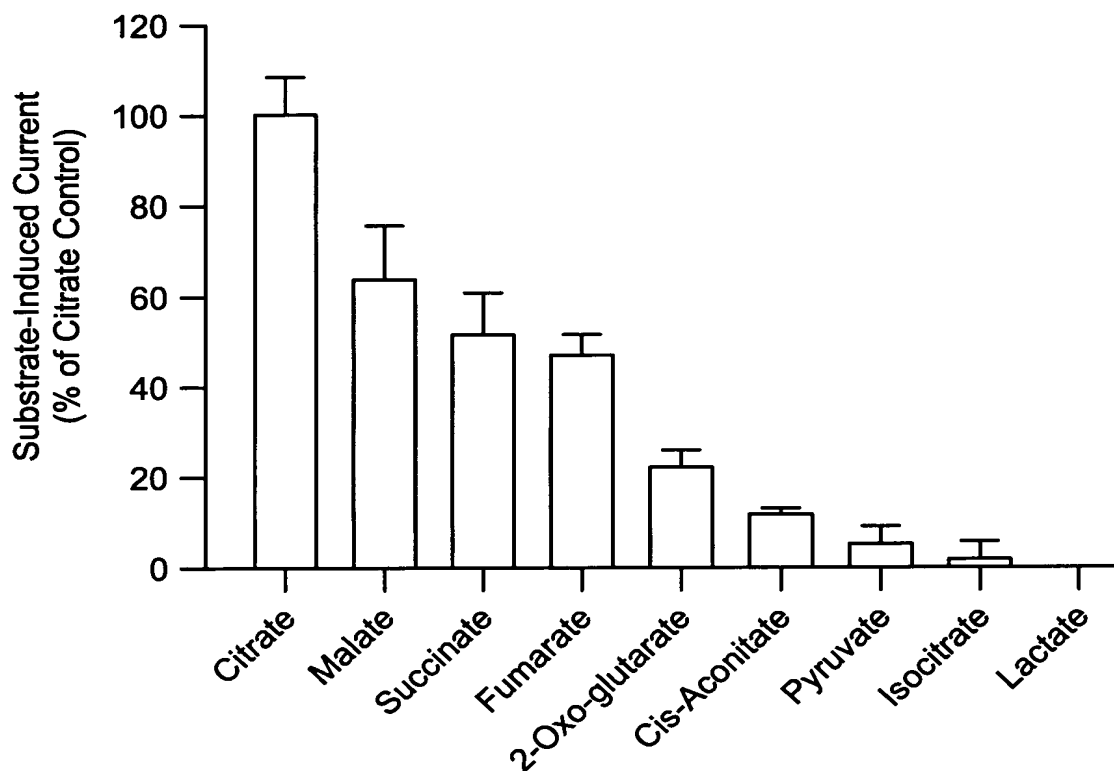
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Fig. 33



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Fig. 34



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Fig. 35A

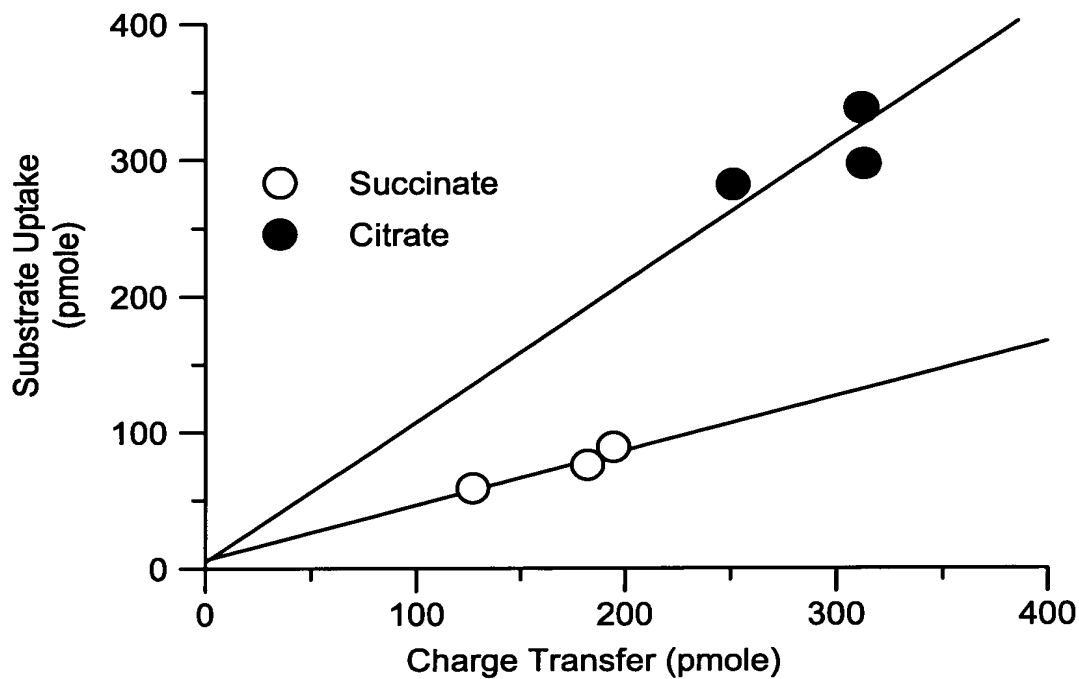
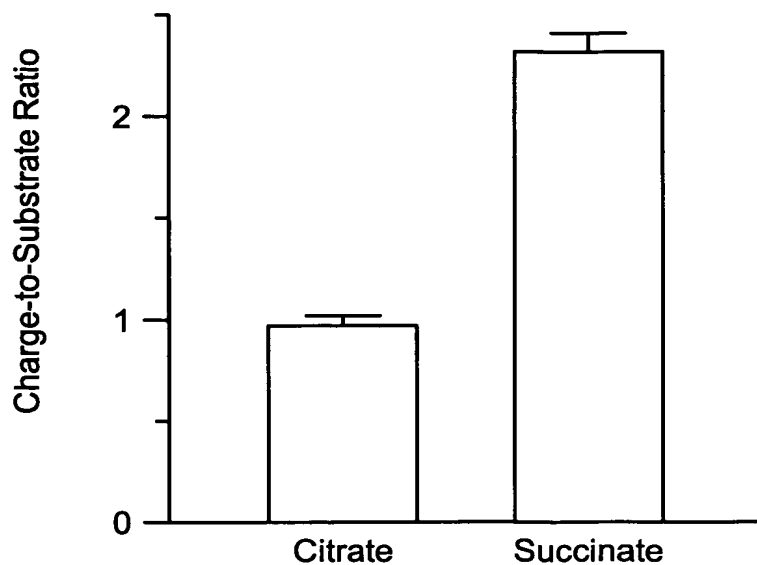


Fig. 35B



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Fig. 36

Zebra Fish NaCT full length cDNA (1#) (1-2536 + 15 bp)

ORF: from 76 – 1824 (length = 1749)

SEQ ID NO: 11

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CCCAAGACGTATGTATGCAGTACCTTAAGGACACTAACATGCTGTTTTCTGGGTGGCCTGATGGTGGCCGTGGCTGT
CGAACACTGGAATCTGCACAAGCGGATCGCCCTGCGGGTGTGCTCCTTGTGGGGGTTCGACCAGCTCTGTTAATG
TTGGGCTTCATGGGTGTAACAGCTTTCTCTCCATGTGGATCAGTAACACGGCCACAACAGCCATGATGGTGCCCA
TCGTT CAGGCAGTTCTCGAGCAGCTCAACAACACAGCACAACAAGAACAAGCTCCATACCTGAGACCGAGGAAAA
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GACCTGAAGAACATTCACGAGAAGCAGAGGAAAGGCTGAAGATGTCTAAAGGCCTGACCTGTGCGTGTGTTATG
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GTTCCCGGACAACCCTGACATCATTAAC TTTGCGTCATGGTTTGGATTTGCCTTTCCAAACATGATCATCATGCTC
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GCTGAGTGTCTTGGCCTCTTCATCTCCTGGTGGTGCTTTGGTTCACTCGTGATCCAGGCTTCGTGGACGGCTGG
GCGACACGCTTCTTCAATGTGACAAAGAGTTTGTGACAGATGCCACGGTTGCAGTGTGTTGTGGCTGCGCTGCTCT
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Amino Acid Sequence (581 aa)

SEQ ID NO: 12

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VQAVLEQLNNTAQEQSSIPETEEKSTEKQPESPGEEKVVLNGDNFSMESDP EEHSREAEERLKMSKGLTLCVCYA
ASIGGTATLTGTGPNLVLMGQMSQLFPDNPDIINFASWFGFAFPNMIIMLT LAWLWLQIVFLGINFKKTWGCGTVK
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VFPSKPPRLCFWRTE SFDTVPQQESGPTPALLTWKV TQKKMPWSIILLGGGFALAKGSEISGLSKWLGDQMSPLQ
SIPPWAI AIVICLMIATFTECTSNVATATLFLPILASMSQSIGVNPLYVMVPCTLSASFAMLPVATPPNAIVFSY
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Fig. 37

fish	1	MASRALKLVWKMNTLLILECTPFLLLPLPLVIGSKEAGCAYVVVLMAVYWCTEVLPIAVT
mouse	1	-MSAKTCVTKFKSFALLFTPIILMLPLVILIPDKFARCAIVIVIMAVYWCTDVIPVAVT
rat	1	-MASAKTYVTKFKSFVILFFAPILLPLILVDPKFAVCAYVILMATYWCTDVIPVAIT
human	1	-MASALSYVSKFKSFVILEFTPLLLPLVLILMPAKFVRCAYVILMATYWCTEVIPIAVT
fish	61	ALLPAVLFPFLFRIMESQVCMQYLKDTNMLFLGCLMVAVAVEHWNLHKRIALRVLLLVGV
mouse	60	SLLPVLLFPLLKVLDSKQVCIQYMKDTNMLFLGSLIVAVAVRWLHKRVLRMLLFVGT
rat	60	SLLPVLLFPLLKVLDSKQVCVQYMTDTNMLFLGSLIVATAVERWELHKRIALRMLLFVGT
human	60	SLMPVLLFPLFQILDSRQVCVQYMKDTNMLFLGCLIVAVAVRWNLHKRIALRTLWVGA
fish	121	RPALMLLGMGVTAFLSMWISNTATTAMVPIVQAVLEQLNNTAQQEQSSIPETEEKSTE
mouse	120	KPSRLMLGFMFVTAFLSMWISNTAATAMMIPIVEAMLOQMIAANTAVEASLGTELLDKN
rat	120	KPSRLMLGFMFVTAFLSMWISNTATTAMMIPIVEAMLEQMVATNVAVDASQRTMELLDKN
human	120	KPARLMLGFMGVTAILSMWISNTATTAMVPIVEAILLOQMEATSAATEAG---LELVDKG
fish	181	KQESPGEEKVVLNGDNFSMESDPEEHSREAEERLKMSKGLTLCVCYAASIGGTATLTGT
mouse	180	KTSELPGSQVFE-----DPNVQEQEDEETKNMYKAMHLVCVYSASIGGTATLTGT
rat	180	KASELPGSQVFE-----DPSVQEQEDEETKNMYKAMNLVCVYAASIGGTATLTGT
human	177	KAKELPGSQVFE-----GPTLGOQEDQERKRLCKAMTLCICYAASIGGTATLTGT
fish	241	GPNVLLMGQMSQLFPDNDIINFASWFGFAFPNMIIMLTALAWLWLOTVFLGINFKKTWGC
mouse	231	GPNVLLGQMQLFPDSKDVLNYSWFGFAFPNMVMLVLAWLWLOCLYMRHNLKKTCTC
rat	231	GPNVLLGQMQLFPDSKDVNMFASWFAPALPNMLMLVMWLWLCFYMRPNLKKTCTC
human	228	GPNVLLGQMNELFPDSKDLNMFASWFAPAFPNMLVMLLFAWLWLOFVYMRNFNFKKSWGC
fish	301	G-TVKTEKEIAAYNVTKDEHRSLGPMTEGELSVALFILLVVLWFTTRDPGFVDGWATR-F
mouse	291	CGEKKRDTEKIAAYKVLNEEYQKLGSLSYPECNVLFCTLLVILWFSRDPGFMPGWLSTAW
rat	291	CGRKKKDTEKIAASKVLMEEYRKLGLPLSYAECNVLFCTGLLILWFSRDPGFMPGWLSTAW
human	288	GLESKK-NEKAALKVLQEEYRKLGLPLSFAELNVLICFLLVILWFSRDPGFMPGWLTVAW
fish	359	FNADKEFVTDATVAIFVAALLFVFPSPKPPRLCFWRTEFDTVPQQESGPTPALLTWKVTO
mouse	351	VEGNTVHITDATVAIFVAILLFIIPSQPKPFNFSSQTEEERK---TPFYPPALLDWKVAO
rat	351	IEGNTKHVTDATVAIFVAILLFIVPSQPKPFNFSSQTEEERK---TPFYPPPLLNDWKVTO
human	347	VEGETKYVSDATVAIFVATLLFIVPSQPKPFNFSSQTEEERK---TPFYPPPLLNDWKVTO
fish	419	KKMPWSIILLLLGGGFALAKGSEISGLSKWLGDQMSPLQSIPPWAIATVICLMIATFTECT
mouse	408	EKVPWDIVLLLLGGGFAMAKGCETSGLSKWMMAQMEPLRLVKPAVITLILSCLVAMTTECT
rat	408	EKVPWGIIVLLLLGGGFAMAKGCETSGLSSEWMARQMEPLSSVRPAIITLILSCLVAMTTECT
human	404	EKVPWGIIVLLLLGGGFALAKGSEASGLSVWMGKQMEPLHAVPPAAITLILSLLVAVTECT
fish	479	SNVATATLFLPILASMSQSIGVNPLYVMVPCTLSASFAMLPVATPPNAIVFSYGYLKVS
mouse	468	SNVATTTLFLPIFASMARSGIHPLYVMIPCTMSASLAFMLPVATPPNAIVFAYGHLRVV
rat	468	SNVATTTLFLPIFASMARSGIHPLYVMIPCTLSASLAFMLPVATPPNAIVFAYGHLKVI
human	464	SNVATTTLFLPIFASMSRSIGLNPLYIMLPCTLSASFAMLPVATPPNAIVFYGHLKVA
fish	539	DMVKTGIVMNIIGILSITLAINSWGRAIFSLDTPPSWANTTDV--
mouse	528	DMVKTGLIMNFVIGILSVFLSVNTWGRAMFNLDNFPDWANSTSVNT
rat	528	DMVKTGLVMNIIIGIASVFLSVNTWGRAVFNLDKFPDWANLTHINT
human	524	DMVKTGVIMNIIIGVFCVFLAVNTWGRAIFDLDFPDWANVTHIET

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Fig. 38A

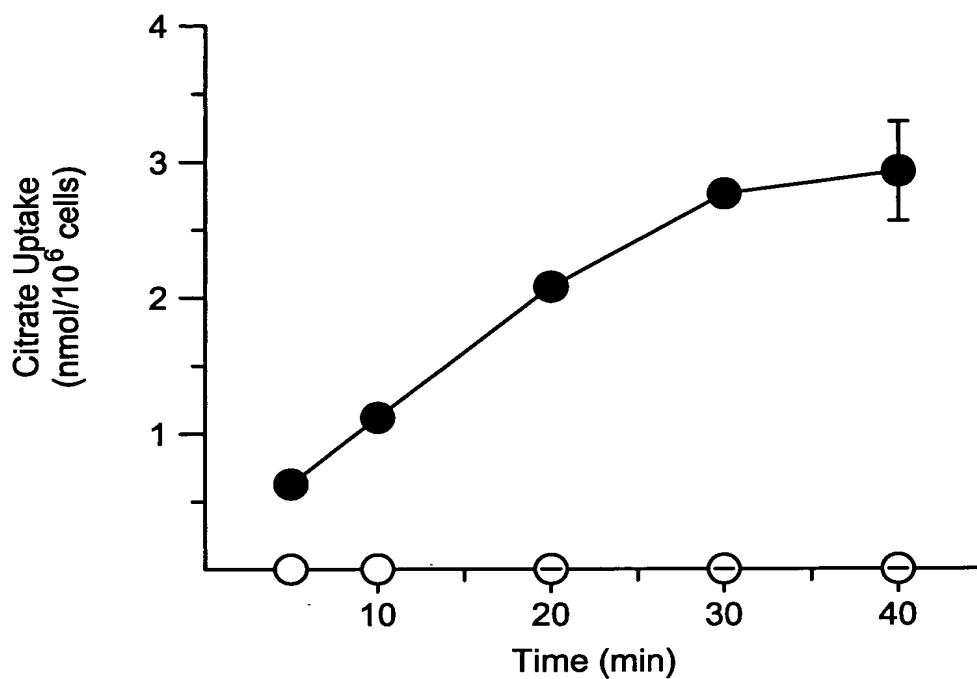
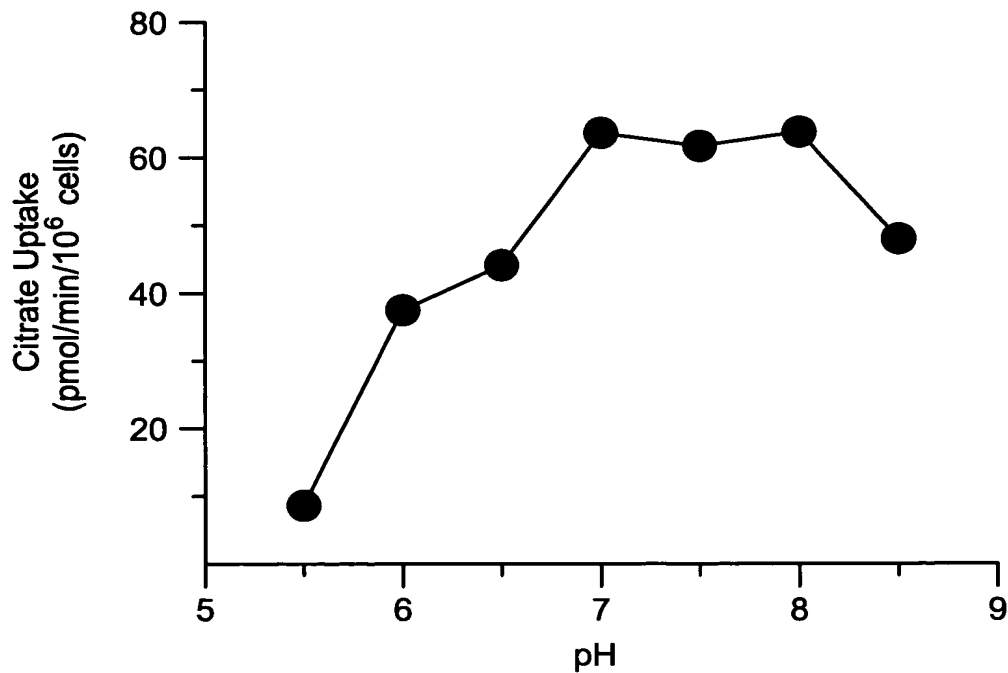


Fig. 38B



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Fig. 39A

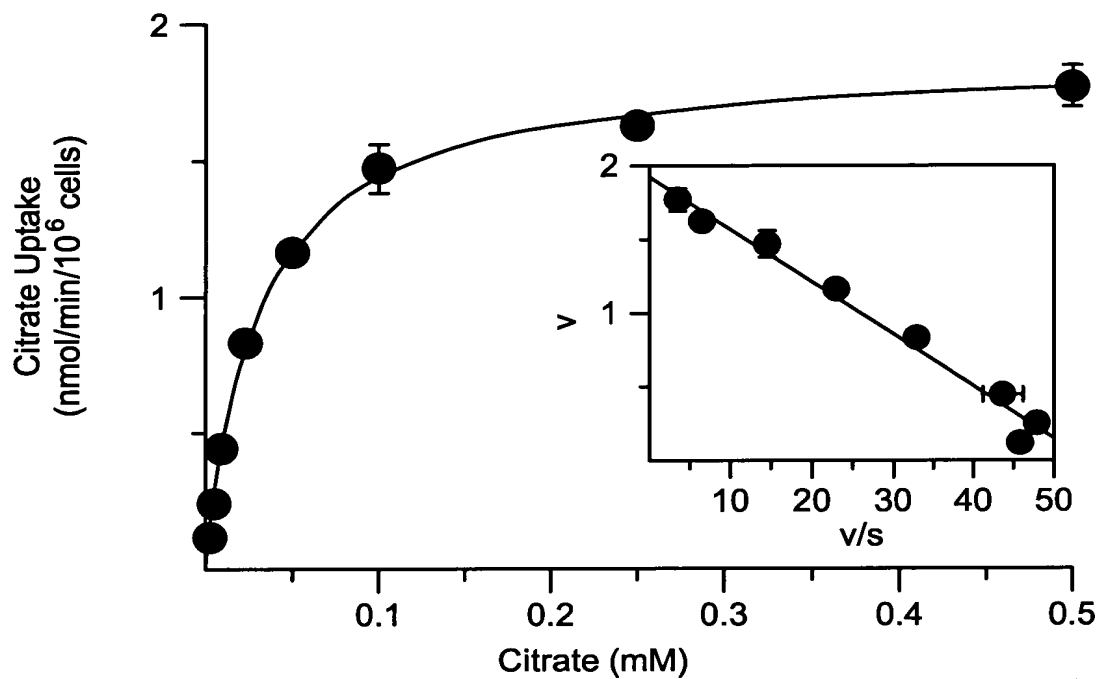
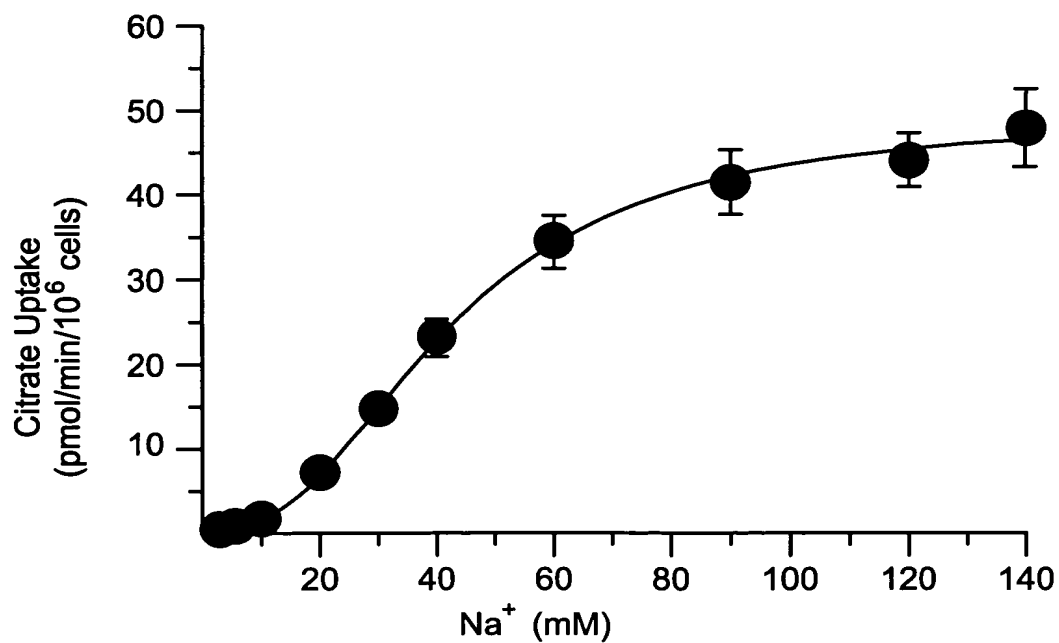


Fig. 39B



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Fig. 40A

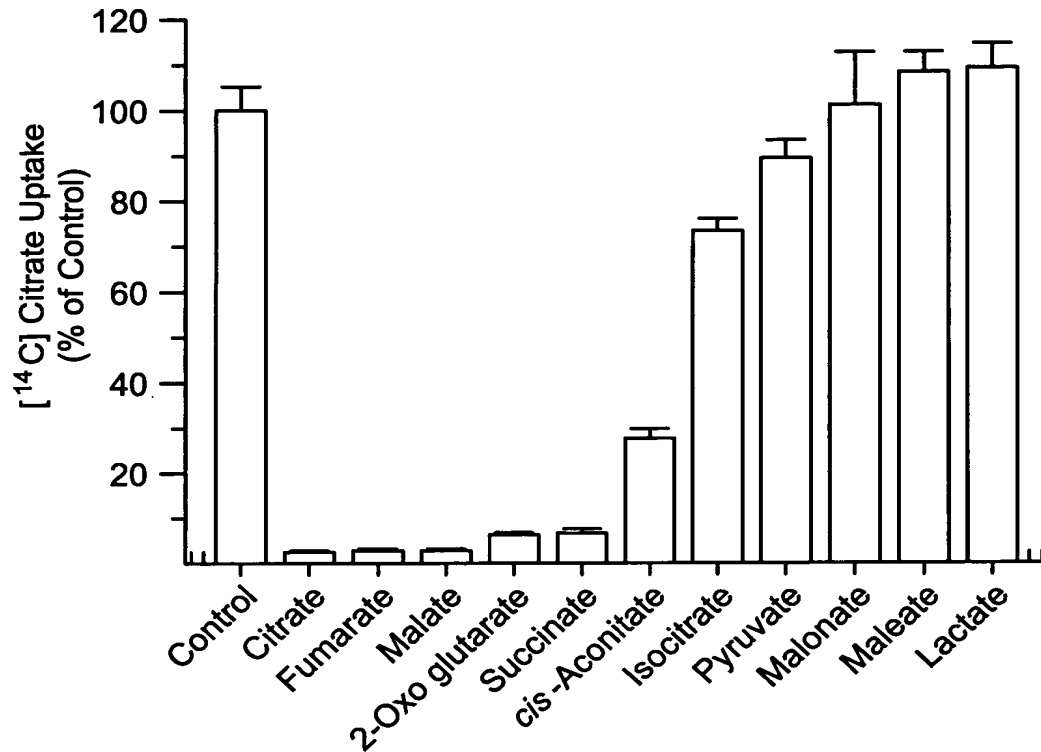
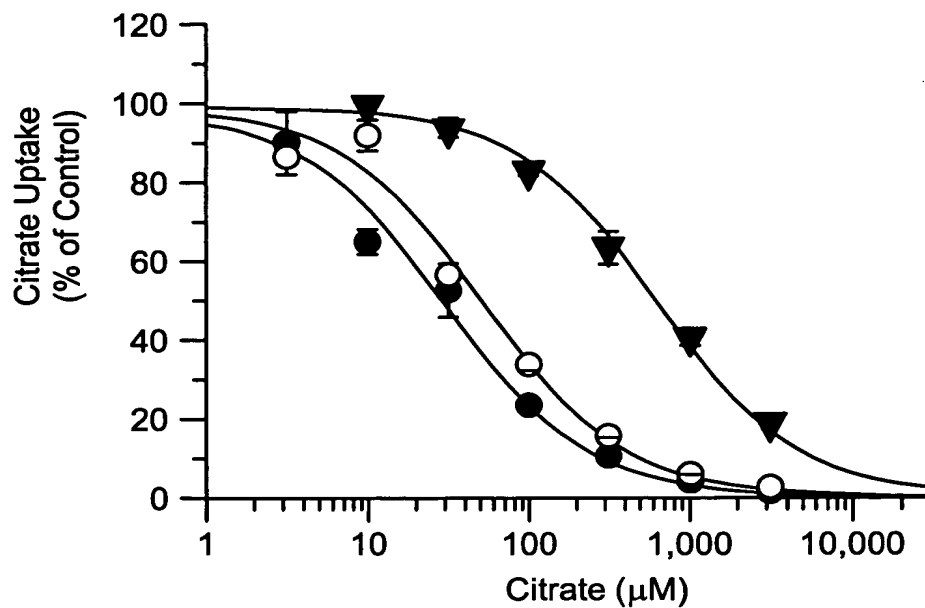
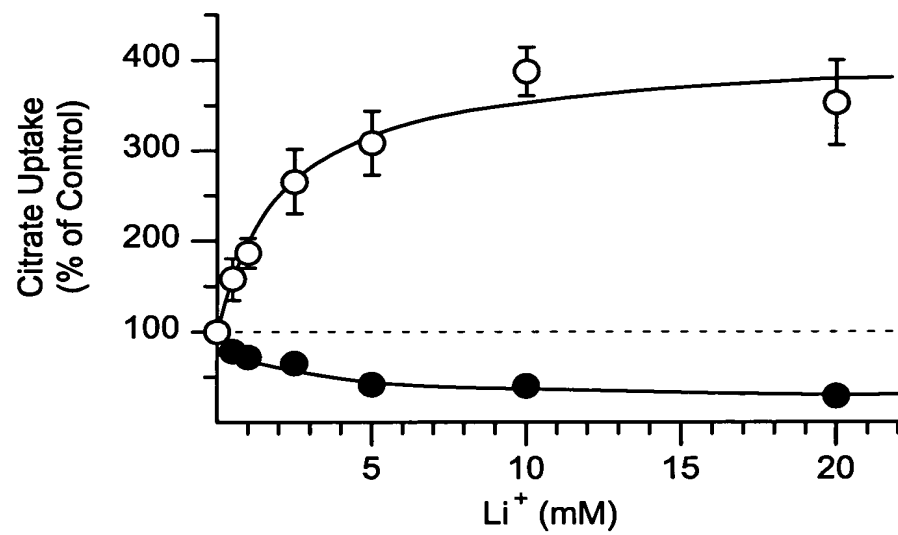


Fig. 40B



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Fig. 41



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Fig. 42A

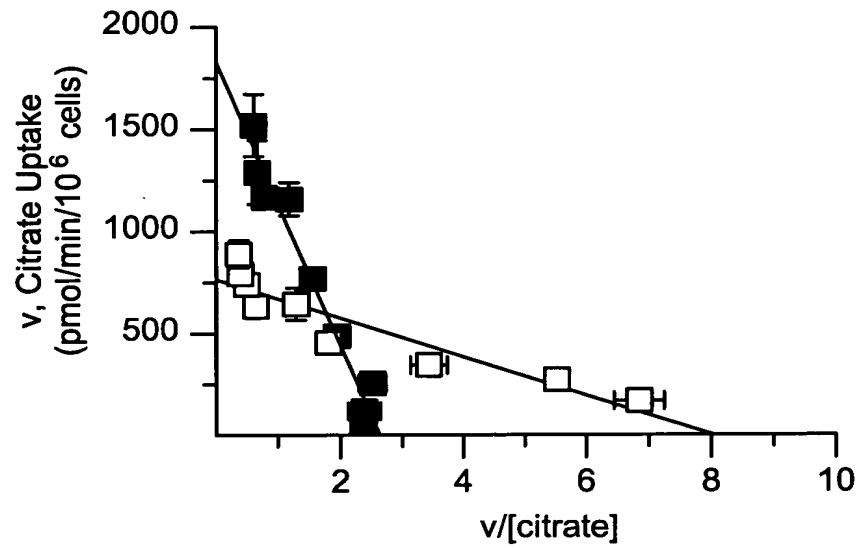
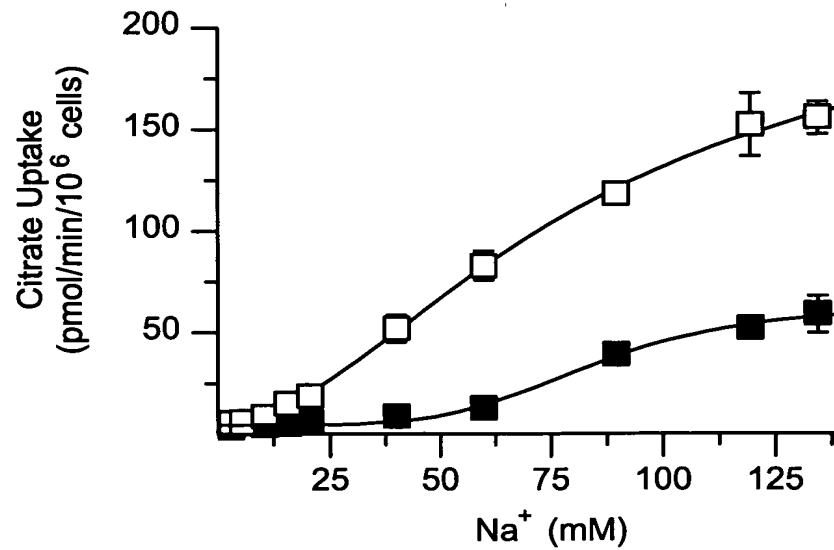


Fig. 42B



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Fig. 43A

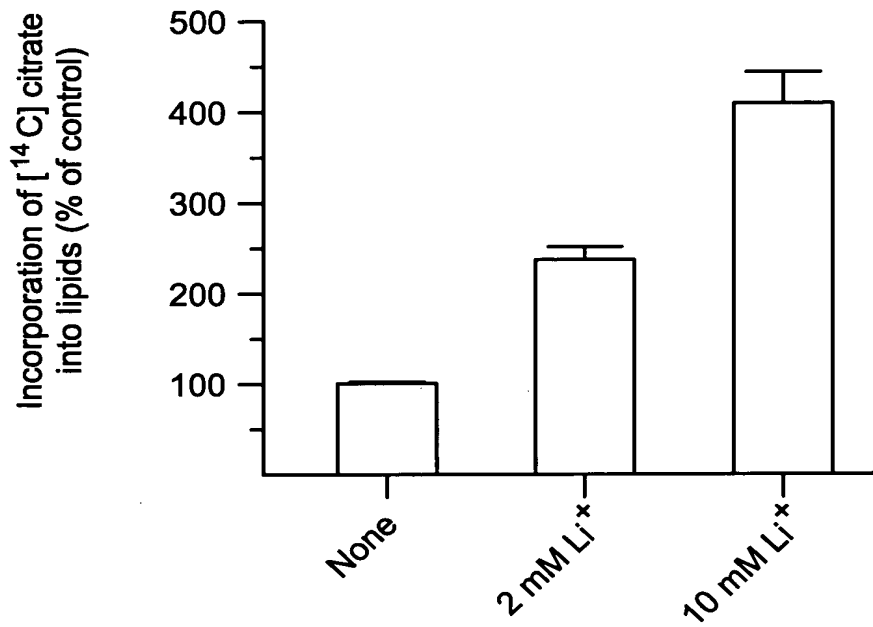
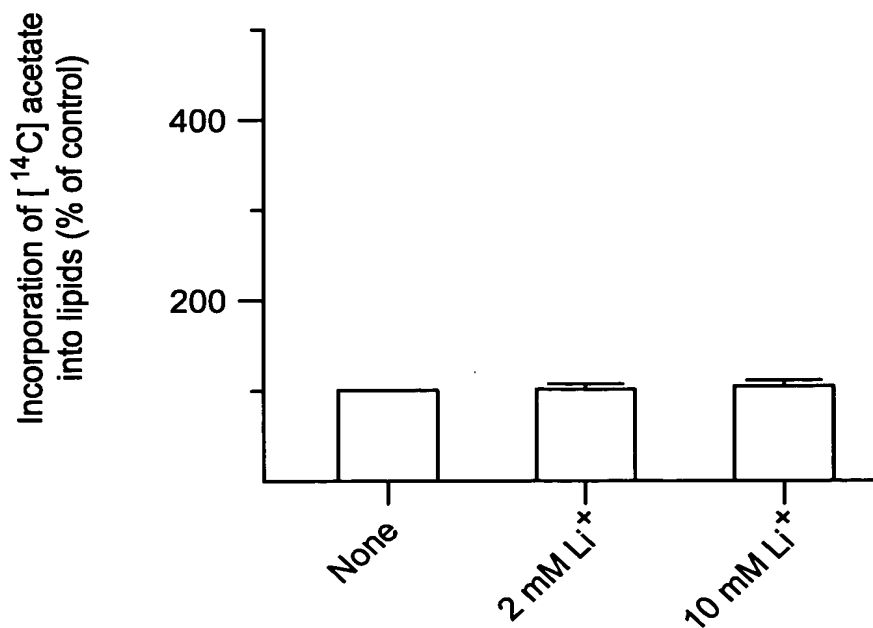


Fig. 43B



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Fig. 44A




		-Li ⁺	+Li ⁺	ratio
		<i>Citrate uptake</i> (pmol/min/10 ⁶ cells)		
human		21.8 ± 2.5	70.5 ± 4.6	3.23
rat		88.7 ± 6.5	21.8 ± 2.5	0.42
chimera		116.4 ± 5.3	111.1 ± 5.0	0.95

Fig. 44B

human 500 LSASFAMLPVATPPNAIVFT 516
 rat LSASLAFMLPVATPPNAIVFA 520
 504

Fig. 44C

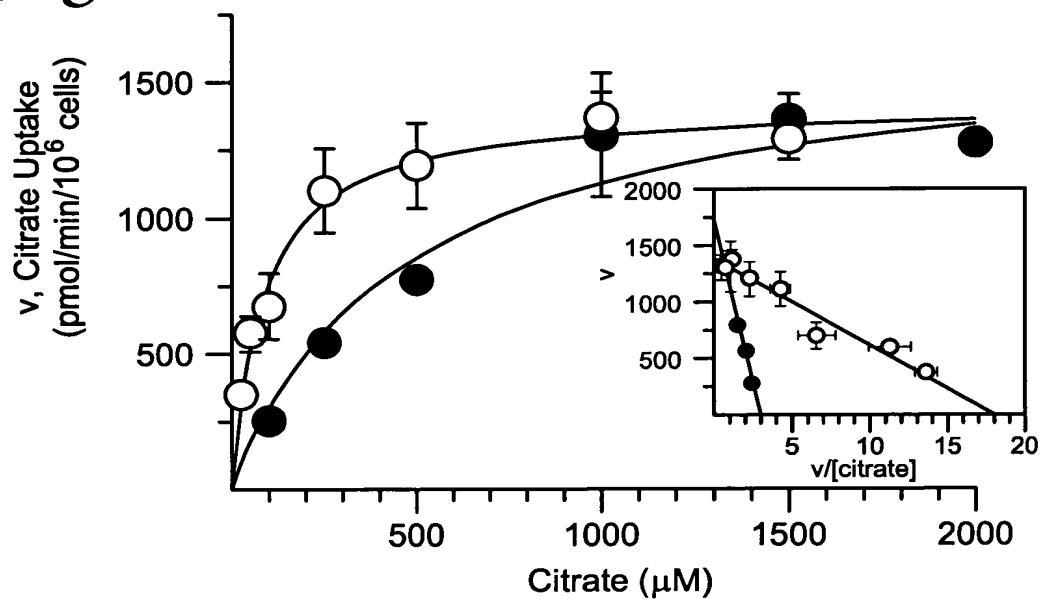


Fig. 44D

